



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jan 31, 2017 – 12:43 PM EST

PDB ID : 3JBV
EMDB ID: : EMD-6486
Title : Mechanisms of Ribosome Stalling by SecM at Multiple Elongation Steps
Authors : Zhang, J.; Pan, X.J.; Yan, K.G.; Sun, S.; Gao, N.; Sui, S.F.
Deposited on : 2015-10-16
Resolution : 3.32 Å (reported)
Based on PDB ID : 4V7T

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

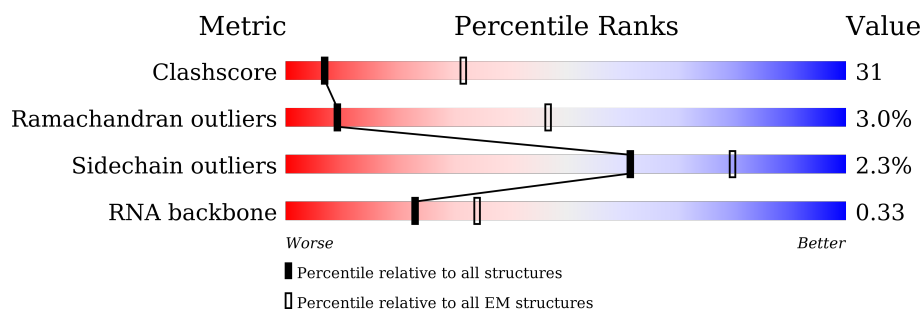
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.32 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




























Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1542	42% 39% 17% .
2	B	241	57% 31% . 10%
3	C	233	53% 33% . 12%
4	D	206	56% 43%
5	E	167	55% 31% . 10%
6	F	131	48% 28% 24%
7	G	156	67% 27% . .
8	H	130	66% 33% .


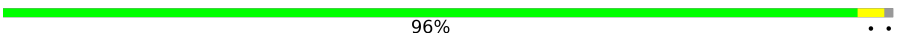

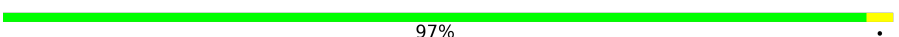

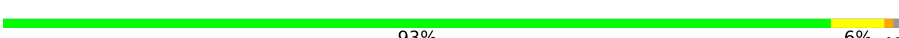




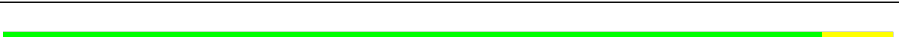


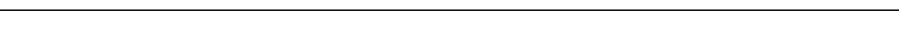
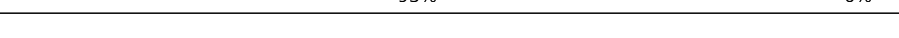
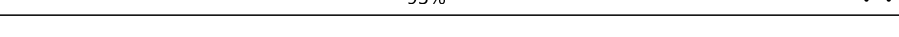
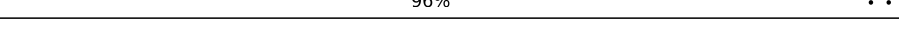
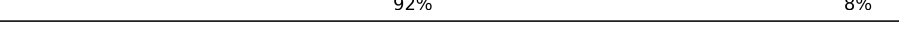
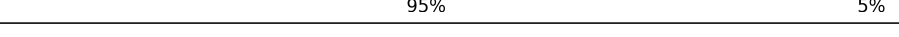
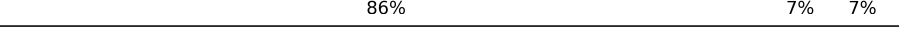

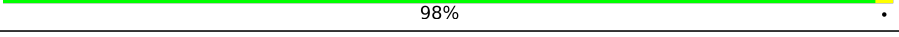

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Mol	Chain	Length	Quality of chain
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	V	76	
23	W	75	
24	X	11	
25	0	78	
26	1	63	
27	2	59	
28	3	57	
29	4	55	
30	6	46	
31	7	65	
32	8	38	
33	a	120	

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Mol	Chain	Length	Quality of chain
34	b	2904	
35	c	273	
36	i	142	
37	d	209	
38	e	201	
39	f	179	
40	g	177	
41	h	149	
42	j	142	
43	k	123	
44	l	144	
45	m	136	
46	n	127	
47	o	117	
48	p	115	
49	q	118	
50	r	103	
51	s	110	
52	t	100	
53	u	104	
54	w	94	
55	y	85	
56	z	27	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145911 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called RNA (1530-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	113	Total	C	N	O	S	0	0
			876	541	177	155	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	79	ARG	GLN	ENGINEERED MUTATION	UNP P0ADZ4

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 22 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	76	Total	C	N	O	P	0	0
			1620	723	290	532	75		

- Molecule 23 is a RNA chain called RNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	75	Total	C	N	O	P	0	0
			1599	713	287	525	74		

- Molecule 24 is a RNA chain called RNA (5'-R(P*CP*UP*GP*GP*CP*CP*CP*UP*CP*A P*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	11	Total	C	N	O	P	0	0
			231	103	39	78	11		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 33 is a RNA chain called RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	117	Total	C	N	O	P	0	0
			2506	1116	459	814	117		

- Molecule 34 is a RNA chain called RNA (2903-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 35 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 36 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	134	Total	C	N	O	S	0	0
			976	614	169	187	6		

- Molecule 37 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 38 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 39 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 40 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 41 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	h	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 42 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 43 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 44 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 45 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	135	Total	C	N	O	S	0	0
			1063	680	201	176	6		

- Molecule 46 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 47 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 48 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 49 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 50 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 51 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 52 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 53 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 54 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

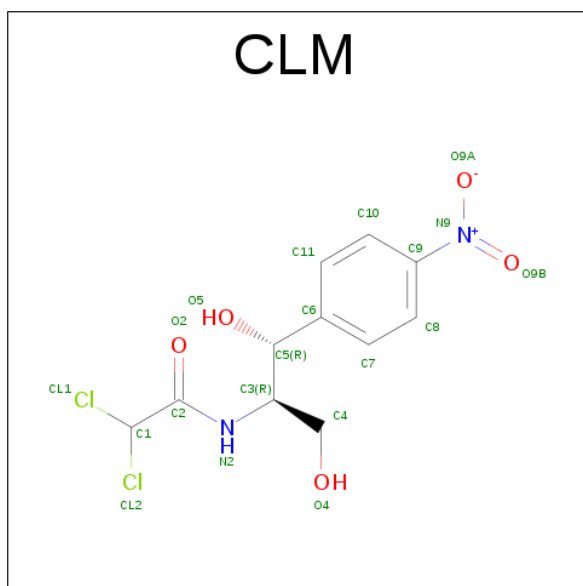
- Molecule 55 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 56 is a protein called Secretion monitor.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	z	27	Total	C	N	O	0	0
			211	134	35	42		

- Molecule 57 is CHLORAMPHENICOL (three-letter code: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$).

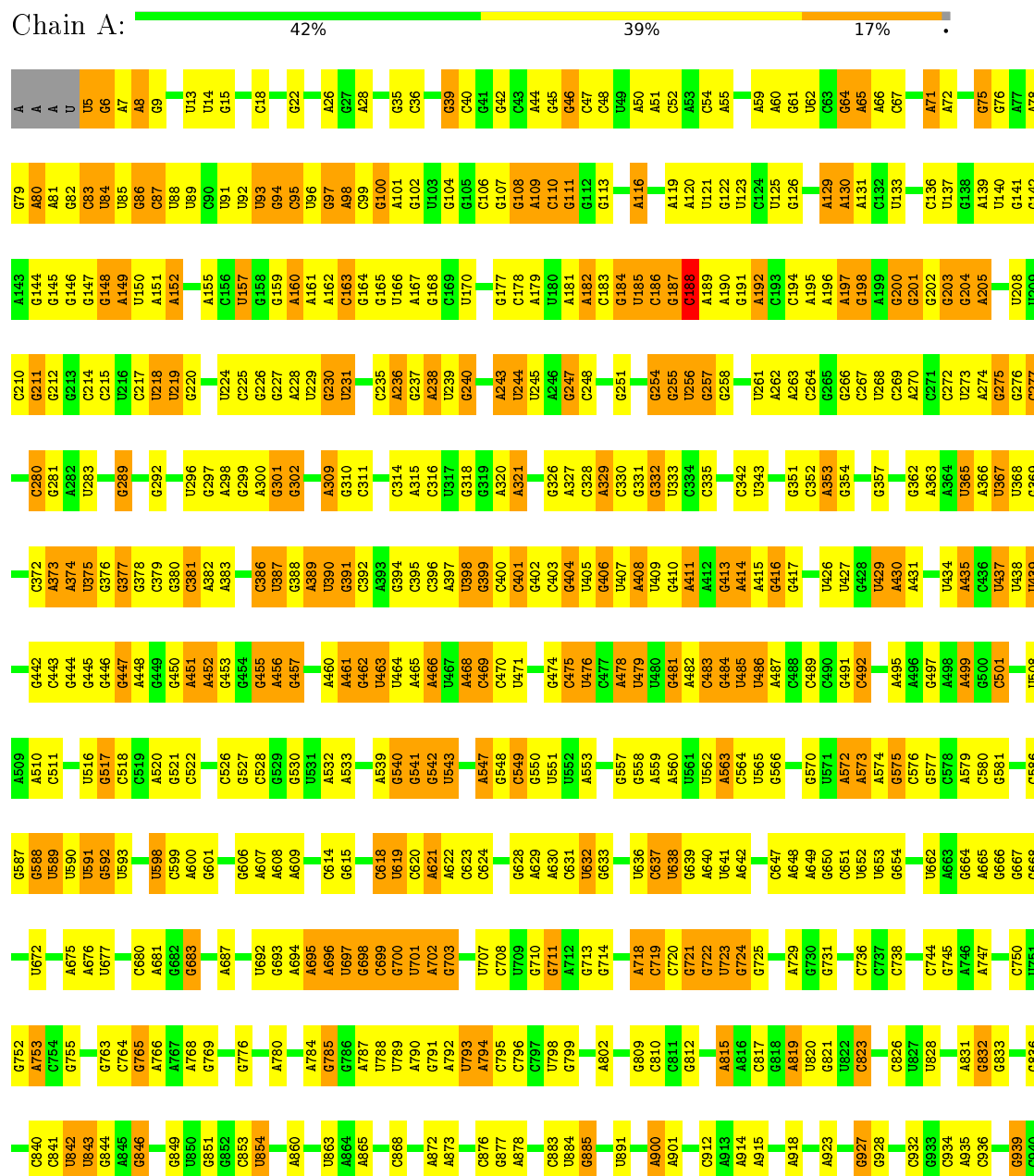


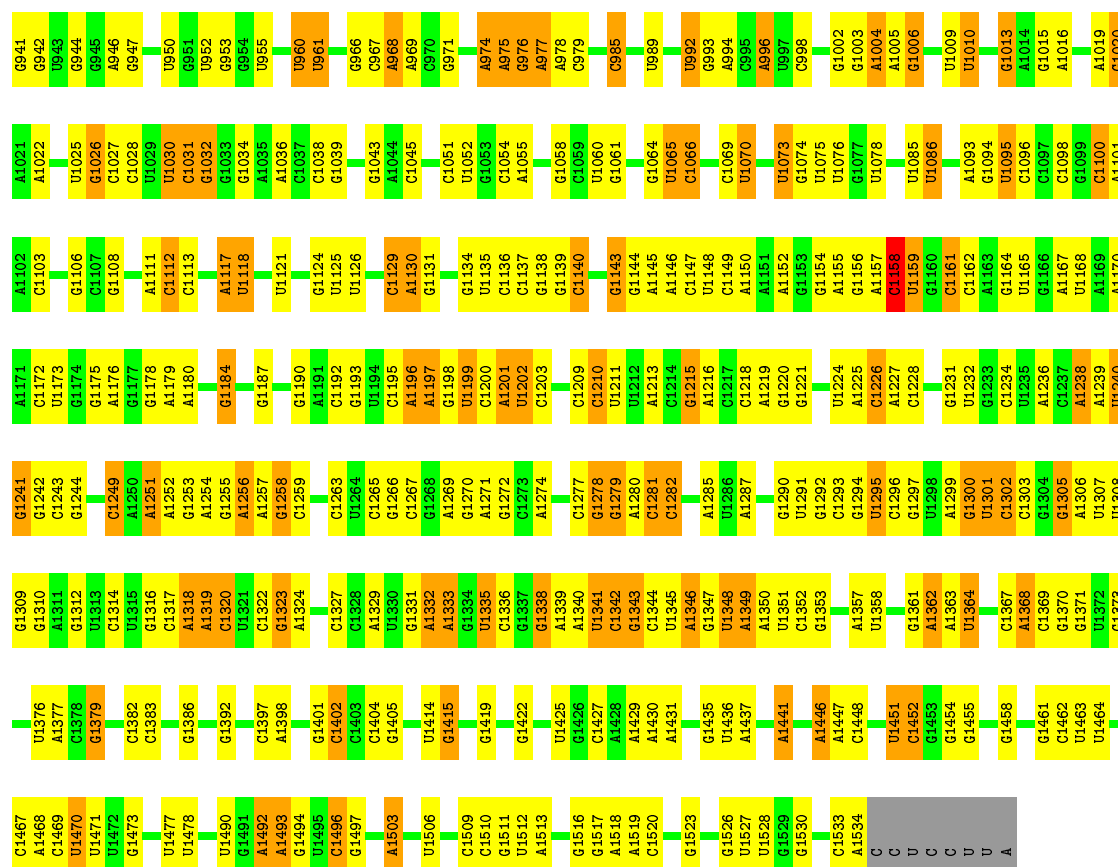
Mol	Chain	Residues	Atoms					AltConf
57	b	1	Total	C	Cl	N	O	0
			20	11	2	2	5	

3 Residue-property plots

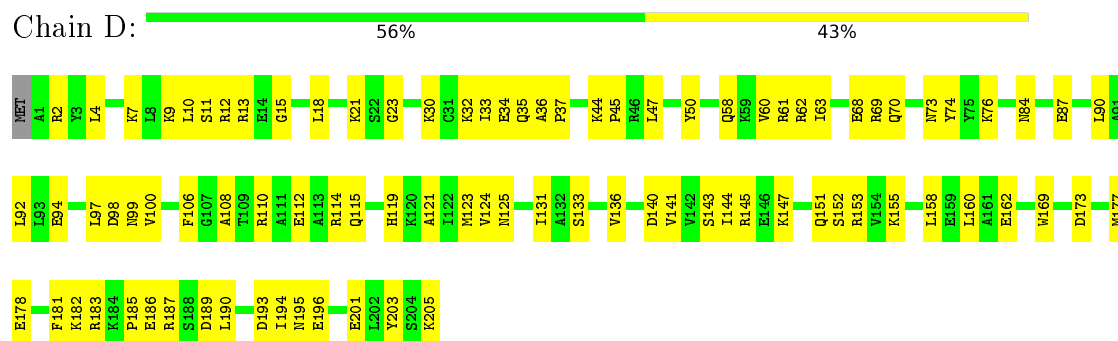
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RNA (1530-MER)

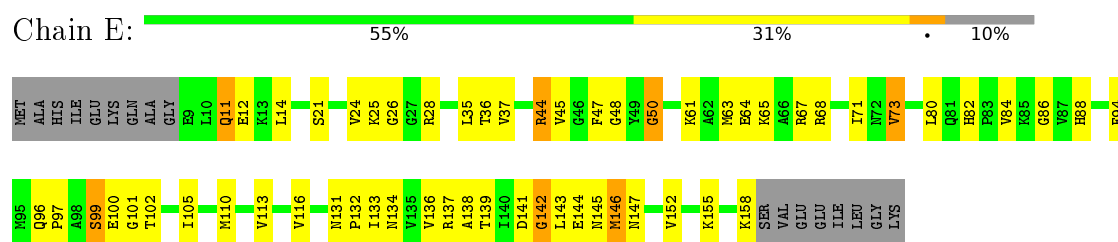




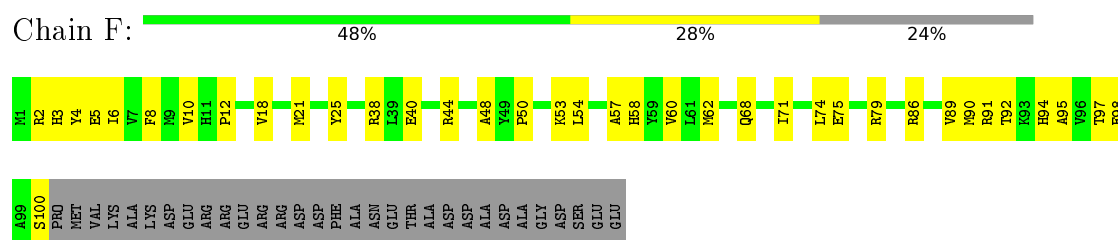
- Molecule 4: 30S ribosomal protein S4



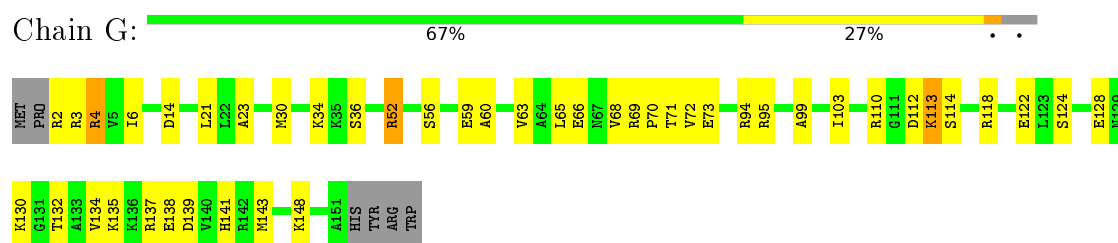
- Molecule 5: 30S ribosomal protein S5



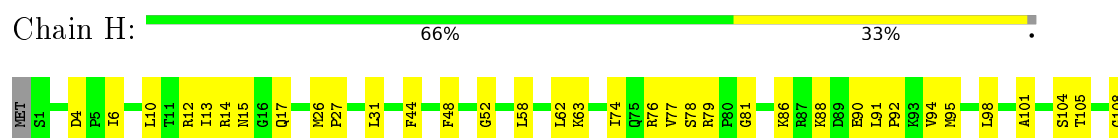
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8

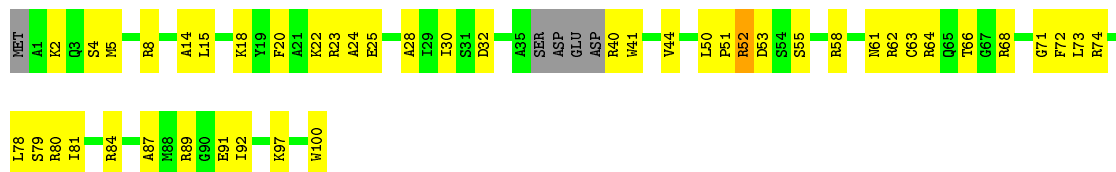






• Molecule 14: 30S ribosomal protein S14

Chain N: 50% 44% 5%



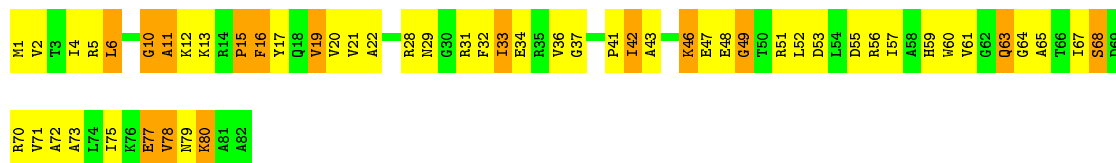
• Molecule 15: 30S ribosomal protein S15

Chain O: 67% 31%



• Molecule 16: 30S ribosomal protein S16

Chain P: 34% 48% 18%



• Molecule 17: 30S ribosomal protein S17

Chain Q: 61% 33% 5%



• Molecule 18: 30S ribosomal protein S18

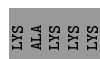
Chain R: 48% 25% 27%



• Molecule 19: 30S ribosomal protein S19

Chain S: 51% 34% 14%





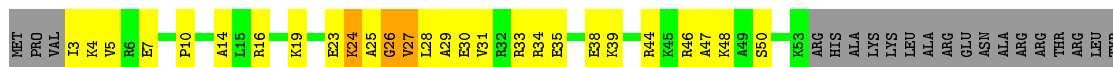
- Molecule 20: 30S ribosomal protein S20

Chain T:  69% 29% .



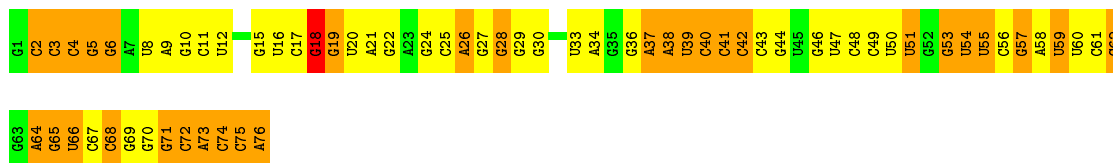
- Molecule 21: 30S ribosomal protein S21

Chain U:  34% 34% 28% .



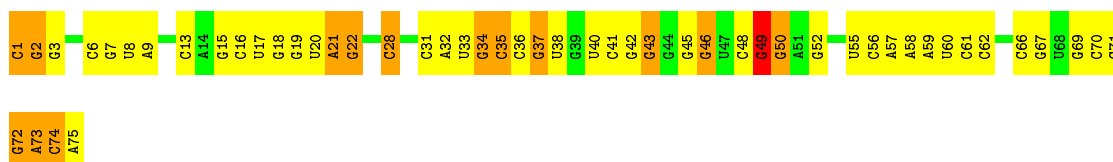
- Molecule 22: RNA (76-MER)

Chain V:  14% 43% 41% .



- Molecule 23: RNA (75-MER)

Chain W:  31% 49% 19% .




- Molecule 24: RNA (5'-R(P*CP*UP*GP*GP*CP*CP*CP*UP*CP*AP*A)-3')

Chain X:  27% 64% 9%




- Molecule 25: 50S ribosomal protein L28

Chain 0:  90% 8% ..



- Molecule 26: 50S ribosomal protein L29

Chain 1:  84% 13% ..




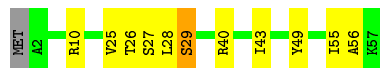
- Molecule 27: 50S ribosomal protein L30

Chain 2:  86% 8% ..




- Molecule 28: 50S ribosomal protein L32

Chain 3:  79% 18% ..




- Molecule 29: 50S ribosomal protein L33

Chain 4:  85% 5% 9%




- Molecule 30: 50S ribosomal protein L34

Chain 6:  89% 7% .



- Molecule 31: 50S ribosomal protein L35

Chain 7:  89% 9% .



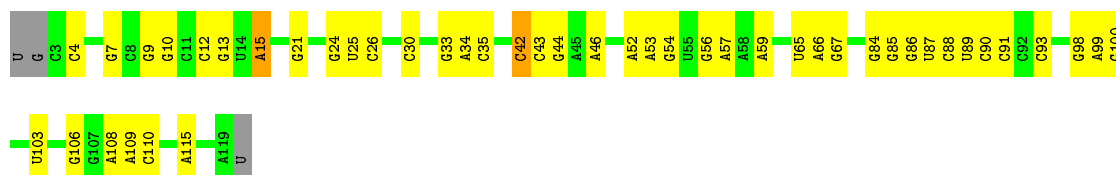
- Molecule 32: 50S ribosomal protein L36

Chain 8:  87% 13%



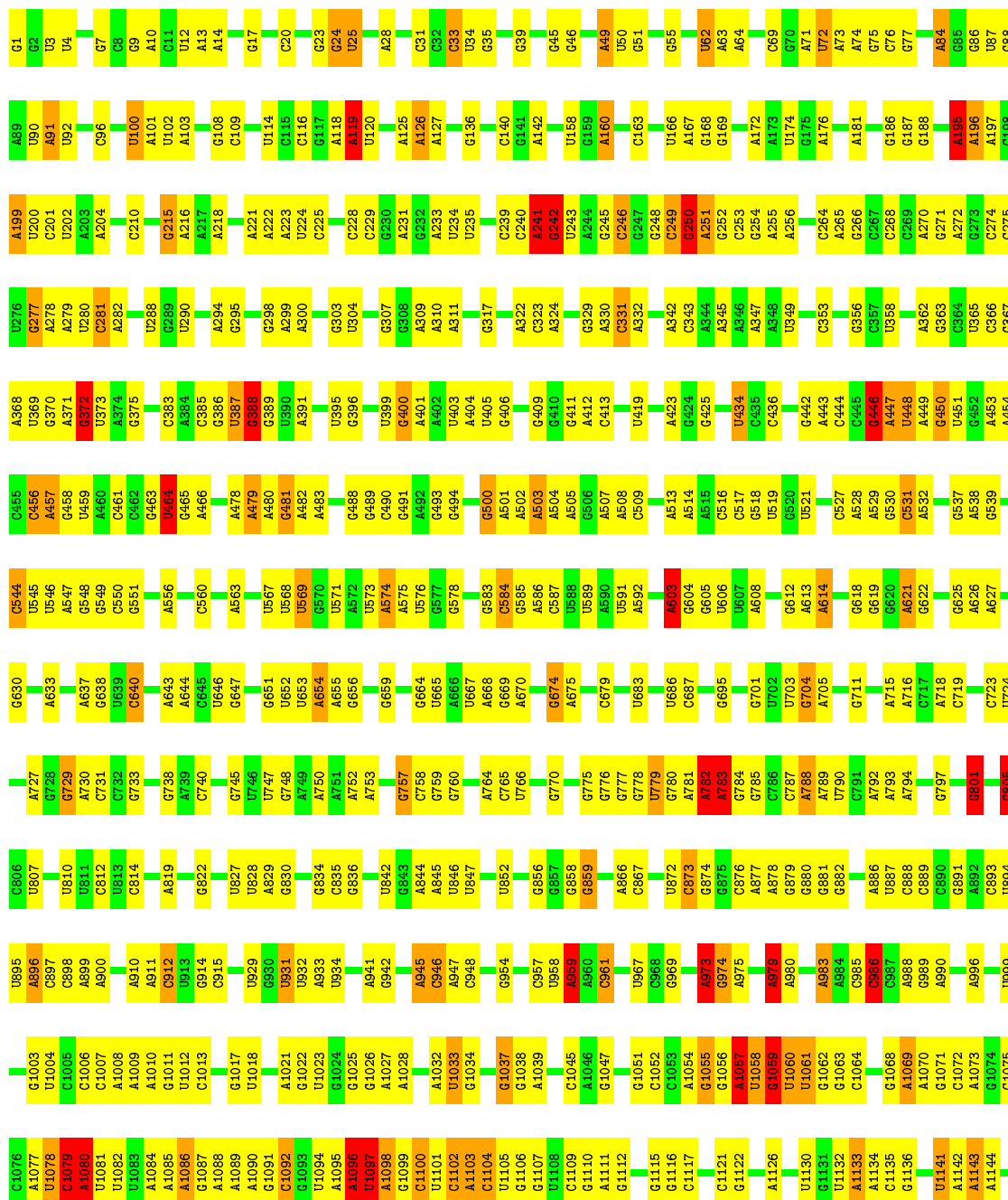
- Molecule 33: RNA (118-MER)

Chain a:  59% 37% ..

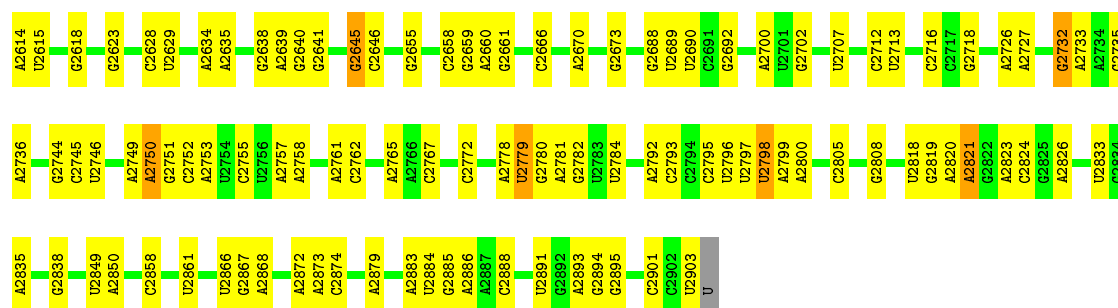


• Molecule 34: RNA (2903-MER)

Chain b: 55% 38% 5%



A2534	A2535	G2536	G2544	A2547	C2551	U2554	C2556	G2557	U2562	U2563	A2564	A2565	A2566	U2567	U2571	A2572	C2573	G2574	C2575	U2576	A2577	U2578	U2582	U2583	U2584	U2585	U2586	A2589	A2590	U2593	G2595	U2596	G2597	A2600	A2601	A2602	G2603	G2607	G2608	U2609	C2610	C2611	U2613						
A1450	A1453	G1454	G1455	C1456	U1457	G1458	A1459	C1465	C1466	U1467	C1468	C1470	A1471	U1472	U1473	U1474	C1475	A1476	U1477	A1478	G1481	A1482	C1483	G1484	G1488	U1489	U1490	C1496	A1497	C1498	U1499	C1502	A1503	U1504	G1505	U1506	C1507	G1508	A1513	C1517	A1518	U1519	G1525	G1526	C1527	U1528	C1529	A1530	
G2279	G2280	A2281	G2282	C2283	A2284	C2285	G2286	A2287	A2288	G2289	G2294	A2297	A2298	G2304	U2305	U2306	G2307	G2308	A2311	U2312	G2316	G2319	U2320	U2321	A2322	U2323	U2324	G2325	C2326	A2327	G2330	C2331	G2332	A2333	U2334	A2335	A2336	A2340	G2345	A2346	C2347	C2350	G2353	C2354	G2357	A2358			
G2361	A2366	G2367	G2371	U2372	A2376	G2379	G2382	U2383	C2385	A2388	G2391	G2396	U2402	C2403	U2404	G2405	A2406	A2407	G2410	A2411	G2413	G2414	G2421	U2422	U2423	A2424	A2425	A2426	G2427	G2428	G2429	A2430	U2431	A2434	A2435	U2439	U2440	U2441	G2445	G2446	G2447	U2449							
C2175	A2176	C2177	C2178	C2179	A2183	U2184	U2185	G2189	G2190	A2191	U2192	G2193	A2198	A2199	U2203	G2204	U2210	A2211	A2212	U2213	C2214	C2215	G2218	A2226	G2238	G2239	U2243	C2248	U2249	G2251	G2252	G2255	G2256	U2257	C2261	U2265	A2266	A2267	A2268	G2271	U2272	A2273	A2274	G2276					
G2279	G2280	A2281	G2282	C2283	A2284	C2285	G2286	A2287	A2288	G2289	G2294	A2297	A2298	G2304	U2305	U2306	G2307	G2308	A2311	U2312	G2316	G2319	U2320	U2321	A2322	U2323	U2324	G2325	C2326	A2327	G2330	C2331	G2332	A2333	U2334	A2335	A2336	A2340	G2345	A2346	C2347	C2350	G2353	C2354	G2357	A2358			
G2361	A2366	G2367	G2371	U2372	A2376	G2379	G2382	U2383	C2385	A2388	G2391	G2396	U2402	C2403	U2404	G2405	A2406	A2407	G2410	A2411	G2413	G2414	G2421	U2422	U2423	A2424	A2425	A2426	G2427	G2428	G2429	A2430	U2431	A2434	A2435	U2439	U2440	U2441	G2445	G2446	G2447	U2449							
A2450	A2453	G2454	G2455	C2456	U2457	G2458	A2459	C2465	C2466	U2467	C2468	C2470	A2471	U2472	U2473	U2474	C2475	A2476	U2477	A2478	G2481	A2482	C2483	G2484	G2488	U2489	U2490	C2496	A2497	C2498	C2499	U2500	G2502	A2503	U2504	G2505	U2506	C2507	G2508	A2513	C2517	A2518	U2519	G2525	G2526	C2527	U2528	C2529	A2530
A2534	A2535	G2536	G2544	A2547	C2551	U2554	C2556	G2557	U2562	U2563	A2564	A2565	A2566	U2567	U2571	A2572	C2573	G2574	C2575	U2576	A2577	U2578	U2582	U2583	U2584	U2585	U2586	A2589	A2590	U2593	G2595	U2596	G2597	A2600	A2601	A2602	G2603	G2607	G2608	U2609	C2610	C2611	U2613						



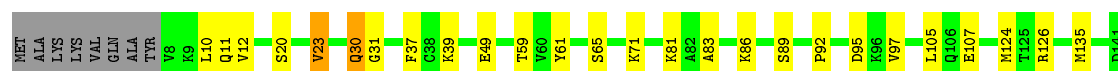
- Molecule 35: 50S ribosomal protein L2

Chain c: 96%



- Molecule 36: 50S ribosomal protein L9

Chain i: 76% 17% 6%



- Molecule 37: 50S ribosomal protein L11

Chain d: 97%



- Molecule 38: 50S ribosomal protein L3

Chain e: 94% 6%



- Molecule 39: 50S ribosomal protein L4

Chain f: 93% 6% ..



- Molecule 40: 50S ribosomal protein L5

Chain g: 95%



- Molecule 41: 50S ribosomal protein L6

Chain h:  97% ..



- Molecule 42: 50S ribosomal protein L13

Chain j:  96% .




- Molecule 43: 50S ribosomal protein L14

Chain k:  95% ..



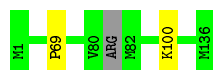
- Molecule 44: 50S ribosomal protein L15

Chain l:  92% 8%




- Molecule 45: 50S ribosomal protein L16

Chain m:  98% ..



- Molecule 46: 50S ribosomal protein L17

Chain n:  91% 6%



- Molecule 47: 50S ribosomal protein L18

Chain o:  93% 6%



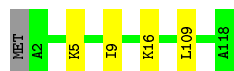
- Molecule 48: 50S ribosomal protein L19

Chain p:  95% ..



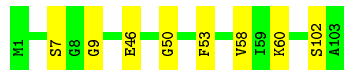
- Molecule 49: 50S ribosomal protein L20

Chain q:  96% ..



- Molecule 50: 50S ribosomal protein L21

Chain r:  92% 8%




- Molecule 51: 50S ribosomal protein L22

Chain s:  95% 5%




- Molecule 52: 50S ribosomal protein L23

Chain t:  86% 7% 7%



- Molecule 53: 50S ribosomal protein L24

Chain u:  84% 14% .




- Molecule 54: 50S ribosomal protein L25

Chain w:  98% .



- Molecule 55: 50S ribosomal protein L27

Chain y:  87% . 12%



● Molecule 56: Secretion monitor



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	60354	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	37878	Depositor
Image detector	GATAN K2 Summit (4K X 4K)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CLM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 2$	RMSZ	# $ Z > 2$
1	A	0.47	0/36762	0.79	8/57350 (0.0%)
10	J	0.29	0/796	0.56	0/1077
11	K	0.28	0/893	0.52	0/1205
12	L	0.32	0/969	0.56	0/1300
13	M	0.27	0/884	0.49	0/1181
14	N	0.30	0/785	0.50	0/1043
15	O	0.30	0/724	0.48	0/966
16	P	0.29	0/659	0.49	0/884
17	Q	0.31	0/657	0.49	0/881
18	R	0.29	0/462	0.50	0/621
19	S	0.30	0/652	0.51	0/877
2	B	0.28	0/1735	0.50	0/2338
20	T	0.31	0/671	0.49	0/888
21	U	0.29	0/430	0.60	0/570
22	V	0.33	0/1810	0.80	3/2821 (0.1%)
23	W	0.35	1/1786 (0.1%)	0.92	6/2784 (0.2%)
24	X	0.87	1/256 (0.4%)	0.81	0/394
25	0	0.41	0/635	0.76	1/848 (0.1%)
26	1	0.35	0/502	0.63	0/667
27	2	0.39	0/453	0.64	0/605
28	3	0.42	0/450	0.80	1/599 (0.2%)
29	4	0.38	0/416	0.61	0/554
3	C	0.32	0/1651	0.53	0/2225
30	6	0.48	0/380	0.86	0/498
31	7	0.40	0/513	0.65	0/676
32	8	0.40	0/303	0.77	0/397
33	a	0.45	1/2802 (0.0%)	0.89	4/4369 (0.1%)
34	b	0.59	84/69800 (0.1%)	1.02	432/108892 (0.4%)
35	c	0.42	0/2121	0.76	2/2852 (0.1%)
36	i	0.24	0/989	0.48	0/1334
37	d	0.39	0/1586	0.67	2/2134 (0.1%)
38	e	0.39	0/1571	0.64	1/2113 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	f	0.39	0/1434	0.66	0/1926
4	D	0.31	0/1665	0.52	0/2227
40	g	0.36	0/1343	0.59	1/1816 (0.1%)
41	h	0.27	0/1122	0.60	1/1515 (0.1%)
42	j	0.39	0/1152	0.63	0/1551
43	k	0.41	0/947	0.71	0/1268
44	l	0.41	0/1062	0.71	0/1413
45	m	0.41	0/1081	0.67	0/1443
46	n	0.42	0/973	0.71	0/1301
47	o	0.38	0/902	0.73	2/1209 (0.2%)
48	p	0.38	0/929	0.67	0/1242
49	q	0.45	0/960	0.74	0/1278
5	E	0.34	0/1118	0.56	0/1504
50	r	0.43	0/829	0.65	0/1107
51	s	0.39	0/864	0.70	0/1156
52	t	0.41	0/744	0.67	1/994 (0.1%)
53	u	0.39	0/787	0.68	0/1051
54	w	0.36	0/766	0.59	0/1025
55	y	0.38	0/576	0.64	0/762
56	z	0.46	1/215 (0.5%)	0.91	1/291 (0.3%)
6	F	0.28	0/835	0.53	0/1128
7	G	0.28	0/1187	0.51	0/1591
8	H	0.32	0/989	0.52	0/1326
9	I	0.31	0/1034	0.58	0/1375
All	All	0.50	88/158617 (0.1%)	0.87	466/237442 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
27	2	0	1
34	b	0	64
35	c	0	1
37	d	0	1
43	k	0	1
44	l	0	1
50	r	0	1
9	I	0	1
All	All	0	71

All (88) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	b	2610	C	O3'-P	18.27	1.83	1.61
34	b	2123	G	C6-N1	17.59	1.51	1.39
34	b	2504	U	O3'-P	16.95	1.81	1.61
34	b	2123	G	N3-C4	16.78	1.47	1.35
34	b	2123	G	N9-C8	14.57	1.48	1.37
34	b	2248	C	O3'-P	14.30	1.78	1.61
34	b	399	U	C5'-C4'	13.61	1.67	1.51
34	b	1323	C	O3'-P	13.24	1.77	1.61
34	b	2131	U	N1-C6	13.03	1.49	1.38
34	b	2131	U	N3-C4	12.28	1.49	1.38
34	b	1585	C	N1-C6	11.40	1.44	1.37
34	b	2123	G	C5-C4	11.24	1.46	1.38
34	b	1096	A	O3'-P	10.45	1.73	1.61
34	b	1382	G	C2-N2	-10.45	1.24	1.34
34	b	1079	C	C2-O2	-10.30	1.15	1.24
24	X	12	C	OP3-P	-10.25	1.48	1.61
34	b	1	G	OP3-P	-9.96	1.49	1.61
34	b	1349	C	C4-N4	-9.60	1.25	1.33
34	b	1585	C	N3-C4	9.25	1.40	1.33
34	b	979	A	O3'-P	9.15	1.72	1.61
34	b	1059	G	C6-O6	-9.06	1.16	1.24
34	b	1654	A	N3-C4	8.92	1.40	1.34
34	b	2506	U	O3'-P	-8.90	1.50	1.61
34	b	1654	A	C6-N1	8.25	1.41	1.35
34	b	2602	A	O3'-P	-8.24	1.51	1.61
34	b	1057	A	O3'-P	8.21	1.71	1.61
34	b	514	A	N3-C4	8.18	1.39	1.34
34	b	1059	G	N9-C4	7.99	1.44	1.38
34	b	674	G	O3'-P	7.92	1.70	1.61
34	b	1059	G	C2-N3	7.79	1.39	1.32
34	b	2123	G	N1-C2	7.78	1.44	1.37
34	b	1349	C	N1-C2	7.74	1.47	1.40
34	b	1654	A	N7-C5	7.71	1.43	1.39
34	b	1654	A	N9-C8	7.68	1.43	1.37
34	b	514	A	N7-C5	7.67	1.43	1.39
34	b	2131	U	C2-O2	7.47	1.29	1.22
34	b	2446	G	O3'-P	7.33	1.70	1.61
34	b	1382	G	N1-C2	-7.25	1.31	1.37
34	b	2575	C	O3'-P	7.22	1.69	1.61
34	b	1079	C	O3'-P	7.12	1.69	1.61
34	b	1382	G	C5-C6	7.10	1.49	1.42
34	b	778	G	O3'-P	7.05	1.69	1.61
34	b	514	A	C6-N1	6.91	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	b	2161	C	O3'-P	6.90	1.69	1.61
34	b	1585	C	C2-O2	6.83	1.30	1.24
34	b	1079	C	C2-N3	-6.78	1.30	1.35
34	b	1059	G	N1-C2	-6.68	1.32	1.37
34	b	779	U	O3'-P	6.66	1.69	1.61
34	b	1079	C	N3-C4	-6.62	1.29	1.33
34	b	1349	C	C2-N3	-6.61	1.30	1.35
34	b	1382	G	C6-N1	-6.59	1.34	1.39
34	b	1058	U	O3'-P	6.46	1.69	1.61
34	b	1266	G	O3'-P	6.44	1.68	1.61
34	b	1773	A	O3'-P	6.43	1.68	1.61
34	b	1061	U	O3'-P	6.38	1.68	1.61
34	b	583	G	O3'-P	6.36	1.68	1.61
34	b	2453	A	O3'-P	6.34	1.68	1.61
33	a	25	U	C2-N3	6.31	1.42	1.37
34	b	1349	C	N3-C4	-6.21	1.29	1.33
34	b	1059	G	N3-C4	6.12	1.39	1.35
34	b	1585	C	C4-C5	6.06	1.47	1.43
34	b	1059	G	C6-N1	-6.00	1.35	1.39
34	b	1186	G	O3'-P	5.98	1.68	1.61
34	b	1058	U	N3-C4	-5.86	1.33	1.38
34	b	2449	U	O3'-P	5.69	1.68	1.61
34	b	1097	U	O5'-C5'	5.67	1.53	1.44
34	b	514	A	N9-C8	5.46	1.42	1.37
34	b	1268	A	O3'-P	5.45	1.67	1.61
34	b	757	G	O3'-P	5.43	1.67	1.61
34	b	2004	G	O3'-P	5.40	1.67	1.61
23	W	36	C	O3'-P	-5.40	1.54	1.61
34	b	2518	A	O3'-P	5.37	1.67	1.61
34	b	2123	G	C6-O6	5.36	1.28	1.24
34	b	760	G	O3'-P	5.34	1.67	1.61
56	z	29	PRO	N-CD	5.34	1.55	1.47
34	b	2578	G	O3'-P	5.30	1.67	1.61
34	b	780	G	O3'-P	5.29	1.67	1.61
34	b	942	G	O3'-P	5.28	1.67	1.61
34	b	331	C	N1-C2	5.25	1.45	1.40
34	b	1096	A	C3'-O3'	5.23	1.49	1.42
34	b	2574	G	O3'-P	5.14	1.67	1.61
34	b	87	U	O3'-P	5.11	1.67	1.61
34	b	17	G	O3'-P	5.10	1.67	1.61
34	b	948	C	O3'-P	5.06	1.67	1.61
34	b	1310	G	O3'-P	5.05	1.67	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	b	331	C	C4-C5	5.04	1.47	1.43
34	b	395	U	O3'-P	5.04	1.67	1.61
34	b	2551	C	O3'-P	5.01	1.67	1.61

All (466) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	36	C	O3'-P-O5'	22.33	146.43	104.00
34	b	2602	A	P-O3'-C3'	15.43	138.22	119.70
34	b	1275	A	N9-C1'-C2'	15.08	133.61	114.00
34	b	1096	A	N9-C1'-C2'	-14.60	95.02	114.00
34	b	400	G	N9-C1'-C2'	14.53	132.89	114.00
34	b	1079	C	O4'-C1'-N1	14.09	119.47	108.20
34	b	1058	U	O4'-C1'-N1	13.73	119.19	108.20
34	b	2123	G	N9-C1'-C2'	13.68	131.78	114.00
34	b	1300	G	N9-C1'-C2'	13.56	131.63	114.00
35	c	156	ARG	NE-CZ-NH2	-12.28	114.16	120.30
34	b	2597	G	N9-C1'-C2'	11.95	129.53	114.00
56	z	28	GLY	C-N-CD	-11.54	95.21	120.60
34	b	1059	G	N3-C2-N2	11.51	127.96	119.90
34	b	2504	U	P-O3'-C3'	11.35	133.31	119.70
34	b	1204	A	N9-C1'-C2'	10.77	128.00	114.00
34	b	959	A	N9-C1'-C2'	10.71	127.92	114.00
34	b	1059	G	C4-N9-C1'	10.71	140.42	126.50
34	b	1349	C	C2-N1-C1'	10.60	130.46	118.80
34	b	979	A	N9-C1'-C2'	-10.57	100.26	114.00
34	b	782	A	N9-C1'-C2'	10.51	127.66	114.00
34	b	2161	C	C2'-C3'-O3'	10.47	132.53	109.50
35	c	156	ARG	NE-CZ-NH1	10.43	125.51	120.30
34	b	2449	U	N1-C1'-C2'	-10.36	100.53	114.00
34	b	1349	C	N1-C2-O2	10.24	125.04	118.90
34	b	2160	C	C2'-C3'-O3'	10.20	131.94	109.50
34	b	1205	A	N9-C1'-C2'	10.14	127.18	114.00
34	b	1667	G	N9-C1'-C2'	-10.04	100.95	114.00
34	b	2454	G	N9-C1'-C2'	-9.94	101.07	112.00
34	b	1059	G	C8-N9-C1'	-9.93	114.09	127.00
23	W	36	C	P-O3'-C3'	9.77	131.42	119.70
23	W	36	C	OP2-P-O3'	-9.72	83.82	105.20
34	b	973	A	N9-C1'-C2'	9.66	126.56	114.00
34	b	2123	G	N9-C4-C5	-9.66	101.54	105.40
34	b	372	G	O4'-C1'-N9	9.62	115.90	108.20
34	b	49	A	N9-C1'-C2'	9.56	126.43	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	2123	G	C4-C5-N7	9.38	114.55	110.80
33	a	33	G	N9-C1'-C2'	-9.34	101.72	112.00
34	b	1266	G	O4'-C1'-N9	9.33	115.67	108.20
34	b	1057	A	N9-C1'-C2'	-9.20	101.88	112.00
34	b	986	C	N1-C1'-C2'	9.19	125.95	114.00
34	b	983	A	N9-C1'-C2'	9.13	125.87	114.00
34	b	2779	U	N1-C1'-C2'	8.96	125.65	114.00
34	b	2161	C	O4'-C4'-C3'	-8.95	95.05	104.00
34	b	1349	C	C6-N1-C1'	-8.89	110.13	120.80
34	b	873	C	C2'-C3'-O3'	8.77	128.78	109.50
34	b	1943	U	N1-C1'-C2'	8.75	125.37	114.00
34	b	242	G	N9-C1'-C2'	-8.69	102.44	112.00
34	b	1930	G	C2'-C3'-O3'	8.67	128.57	109.50
34	b	399	U	N1-C1'-C2'	8.66	125.25	114.00
34	b	1037	G	N9-C1'-C2'	-8.64	102.50	112.00
34	b	246	C	N1-C1'-C2'	8.54	125.10	114.00
34	b	1059	G	N1-C2-N2	-8.33	108.70	116.20
34	b	788	A	N9-C1'-C2'	-8.31	102.85	112.00
34	b	1657	U	C5'-C4'-C3'	8.29	129.27	116.00
34	b	1225	G	N9-C1'-C2'	8.27	124.75	114.00
34	b	2175	C	N1-C1'-C2'	-8.26	102.92	112.00
34	b	2248	C	O3'-P-O5'	-8.22	88.39	104.00
34	b	748	G	O3'-P-O5'	-8.20	88.42	104.00
34	b	614	A	N9-C1'-C2'	8.18	124.63	114.00
34	b	1454	C	N1-C1'-C2'	-8.13	103.06	112.00
34	b	2304	G	C2'-C3'-O3'	8.13	127.39	109.50
34	b	241	A	N9-C1'-C2'	8.12	124.55	114.00
34	b	1069	A	N9-C1'-C2'	-8.12	103.07	112.00
34	b	2266	A	N9-C1'-C2'	8.05	124.46	114.00
34	b	1970	A	N9-C1'-C2'	8.04	124.46	114.00
34	b	1059	G	N1-C6-O6	-8.02	115.09	119.90
34	b	2161	C	C5'-C4'-O4'	8.02	118.73	109.10
34	b	544	C	N1-C1'-C2'	8.02	124.42	114.00
34	b	1657	U	C5'-C4'-O4'	8.01	118.71	109.10
34	b	1943	U	O4'-C1'-N1	-8.00	101.80	108.20
34	b	1967	C	N1-C1'-C2'	7.92	124.30	114.00
34	b	2467	C	N1-C1'-C2'	-7.92	103.29	112.00
34	b	1079	C	N3-C4-N4	-7.91	112.46	118.00
34	b	446	G	N9-C1'-C2'	-7.84	103.38	112.00
34	b	1952	A	N9-C1'-C2'	7.83	124.18	114.00
34	b	974	G	O4'-C1'-N9	7.82	114.46	108.20
34	b	2092	U	N1-C1'-C2'	7.82	124.16	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	1079	C	N3-C2-O2	-7.80	116.44	121.90
34	b	753	A	P-O3'-C3'	-7.79	110.35	119.70
34	b	1392	A	O4'-C1'-N9	7.79	114.43	108.20
34	b	100	U	O4'-C1'-N1	7.78	114.43	108.20
34	b	537	G	N9-C1'-C2'	-7.75	103.47	112.00
34	b	748	G	OP2-P-O3'	7.71	122.17	105.20
34	b	1058	U	N1-C1'-C2'	7.68	123.99	114.00
34	b	1382	G	N1-C6-O6	-7.67	115.30	119.90
34	b	2506	U	OP2-P-O3'	-7.67	88.33	105.20
1	A	1158	C	C2-N1-C1'	7.63	127.19	118.80
34	b	2645	G	N9-C1'-C2'	-7.60	103.64	112.00
34	b	395	U	N1-C1'-C2'	-7.60	103.64	112.00
34	b	2092	U	O4'-C1'-N1	-7.58	102.13	108.20
34	b	25	U	N1-C1'-C2'	7.54	123.81	114.00
34	b	1097	U	O4'-C4'-C3'	-7.52	96.48	104.00
34	b	2032	G	N9-C1'-C2'	7.52	123.77	114.00
34	b	1057	A	C2'-C3'-O3'	7.51	126.02	109.50
34	b	2602	A	OP2-P-O3'	7.49	121.68	105.20
34	b	946	C	C2'-C3'-O3'	7.49	125.97	109.50
34	b	450	G	N9-C1'-C2'	-7.47	103.78	112.00
34	b	464	U	N1-C1'-C2'	7.47	123.72	114.00
34	b	1704	C	C2'-C3'-O3'	7.47	125.94	109.50
34	b	2613	U	N1-C1'-C2'	7.45	123.69	114.00
34	b	2518	A	C2'-C3'-O3'	7.43	125.85	109.50
34	b	1773	A	N9-C1'-C2'	-7.43	103.83	112.00
34	b	1395	A	O4'-C1'-N9	7.41	114.12	108.20
34	b	2449	U	O4'-C1'-N1	7.38	114.10	108.20
34	b	1829	A	N9-C1'-C2'	-7.38	103.89	112.00
34	b	423	A	N9-C1'-C2'	7.37	123.59	114.00
34	b	388	G	O4'-C1'-N9	7.36	114.09	108.20
34	b	167	A	N9-C1'-C2'	7.36	123.57	114.00
34	b	1096	A	C4'-C3'-O3'	7.33	127.67	113.00
34	b	1098	A	O4'-C4'-C3'	-7.33	96.67	104.00
34	b	801	G	O4'-C1'-N9	-7.31	102.35	108.20
34	b	2161	C	C4'-C3'-C2'	-7.29	95.31	102.60
34	b	1932	A	N9-C1'-C2'	7.28	123.47	114.00
34	b	1126	A	N9-C1'-C2'	7.24	123.41	114.00
34	b	2867	G	O4'-C1'-N9	7.24	113.99	108.20
34	b	2123	G	O4'-C1'-N9	7.24	113.99	108.20
34	b	1779	U	O4'-C1'-N1	7.21	113.97	108.20
34	b	479	A	C2'-C3'-O3'	7.21	125.37	109.50
34	b	1382	G	C5-C6-O6	7.21	132.92	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1158	C	N1-C2-O2	7.20	123.22	118.90
34	b	783	A	O5'-P-OP1	-7.19	99.23	105.70
34	b	2518	A	O4'-C1'-N9	-7.15	102.48	108.20
34	b	2051	A	N9-C1'-C2'	-7.13	104.15	112.00
34	b	2439	A	N9-C1'-C2'	-7.13	104.15	112.00
34	b	1698	A	N9-C1'-C2'	7.13	123.27	114.00
34	b	1392	A	C1'-O4'-C4'	-7.12	104.20	109.90
34	b	1395	A	C1'-O4'-C4'	-7.12	104.21	109.90
34	b	729	G	O5'-P-OP1	-7.11	99.30	105.70
34	b	1275	A	O4'-C1'-N9	7.10	113.88	108.20
34	b	783	A	O4'-C1'-N9	7.09	113.88	108.20
34	b	479	A	C4'-C3'-O3'	-7.09	94.52	109.40
34	b	1773	A	C2'-C3'-O3'	7.04	124.98	109.50
34	b	1929	G	N9-C1'-C2'	-7.04	104.26	112.00
34	b	576	U	N1-C1'-C2'	7.03	123.14	114.00
34	b	1037	G	C5'-C4'-O4'	7.02	117.53	109.10
34	b	1272	A	N9-C1'-C2'	7.02	123.12	114.00
34	b	1392	A	N9-C1'-C2'	7.01	123.12	114.00
34	b	2282	G	N9-C1'-C2'	-7.01	104.29	112.00
34	b	2504	U	O3'-P-O5'	-7.01	90.69	104.00
23	W	33	U	O3'-P-O5'	7.00	117.30	104.00
34	b	2530	A	N9-C1'-C2'	6.98	123.08	114.00
34	b	2589	A	N9-C1'-C2'	-6.95	104.36	112.00
34	b	1396	U	C5'-C4'-O4'	6.94	117.43	109.10
34	b	2210	U	N1-C1'-C2'	6.93	123.00	114.00
34	b	1774	C	N1-C1'-C2'	-6.87	104.44	112.00
34	b	531	C	N1-C1'-C2'	6.87	122.93	114.00
34	b	1103	A	O4'-C4'-C3'	-6.86	97.14	104.00
34	b	1103	A	O4'-C1'-N9	6.84	113.67	108.20
34	b	1096	A	C3'-C2'-C1'	6.84	106.97	101.50
34	b	1499	C	N1-C1'-C2'	-6.83	104.49	112.00
34	b	1079	C	C5-C4-N4	6.82	124.98	120.20
34	b	2272	U	N1-C1'-C2'	6.80	122.84	114.00
37	d	4	LEU	CB-CG-CD2	-6.79	99.45	111.00
34	b	1311	G	N9-C1'-C2'	-6.78	104.54	112.00
34	b	388	G	C1'-O4'-C4'	-6.75	104.50	109.90
34	b	199	A	O4'-C1'-N9	6.73	113.59	108.20
1	A	188	C	N1-C2-O2	6.73	122.94	118.90
34	b	2504	U	OP1-P-O3'	6.72	119.98	105.20
34	b	931	U	N1-C1'-C2'	6.71	122.73	114.00
34	b	704	G	C4'-C3'-O3'	6.70	126.39	113.00
34	b	912	C	N1-C1'-C2'	6.68	122.69	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	1168	G	C2'-C3'-O3'	6.68	124.39	113.70
34	b	202	U	N1-C1'-C2'	6.66	122.66	114.00
34	b	2340	A	N9-C1'-C2'	6.66	122.66	114.00
34	b	1754	A	N9-C1'-C2'	6.66	122.66	114.00
34	b	1775	U	N1-C1'-C2'	-6.65	104.68	112.00
34	b	989	G	N9-C1'-C2'	-6.63	104.70	112.00
34	b	674	G	N9-C1'-C2'	-6.63	104.71	112.00
34	b	1996	C	N1-C1'-C2'	6.63	122.61	114.00
34	b	748	G	P-O3'-C3'	6.61	127.63	119.70
34	b	2499	C	C4'-C3'-O3'	6.61	126.21	113.00
34	b	9	G	C2'-C3'-O3'	6.59	124.25	113.70
34	b	481	G	O4'-C1'-N9	6.58	113.47	108.20
34	b	1569	A	N9-C1'-C2'	6.58	122.56	114.00
34	b	1567	G	N9-C1'-C2'	6.55	122.52	114.00
34	b	2123	G	N3-C4-C5	6.55	131.88	128.60
34	b	2336	A	N9-C1'-C2'	6.54	122.50	114.00
34	b	2879	A	N9-C1'-C2'	6.54	122.50	114.00
34	b	2526	G	N9-C1'-C2'	-6.53	104.82	112.00
34	b	1092	C	N1-C1'-C2'	6.52	122.48	114.00
34	b	1058	U	C1'-O4'-C4'	-6.51	104.69	109.90
34	b	2097	A	C2'-C3'-O3'	6.50	124.11	113.70
34	b	1779	U	C1'-O4'-C4'	-6.50	104.70	109.90
34	b	1133	A	O4'-C1'-N9	6.50	113.40	108.20
34	b	1349	C	N3-C2-O2	-6.49	117.36	121.90
34	b	2161	C	C4'-C3'-O3'	6.47	125.94	113.00
34	b	1396	U	C5'-C4'-C3'	6.46	126.34	116.00
34	b	1057	A	C4'-C3'-C2'	-6.46	96.14	102.60
34	b	603	A	O4'-C1'-N9	-6.44	103.05	108.20
34	b	168	G	C2'-C3'-O3'	6.43	124.00	113.70
1	A	188	C	C2-N1-C1'	6.42	125.86	118.80
34	b	2248	C	OP2-P-O3'	6.42	119.32	105.20
34	b	1097	U	C5'-C4'-C3'	6.42	126.27	116.00
34	b	805	G	N9-C1'-C2'	6.41	122.34	114.00
34	b	1616	A	C5'-C4'-O4'	6.41	116.80	109.10
34	b	1458	U	N1-C1'-C2'	6.41	122.33	114.00
34	b	608	A	N9-C1'-C2'	6.41	122.33	114.00
34	b	630	G	N9-C1'-C2'	-6.41	104.95	112.00
34	b	1238	G	N9-C1'-C2'	-6.41	104.95	112.00
34	b	49	A	C8-N9-C1'	-6.40	116.18	127.70
34	b	503	A	C5'-C4'-O4'	6.39	116.77	109.10
34	b	961	C	O5'-P-OP2	-6.37	99.96	105.70
34	b	448	U	N1-C1'-C2'	-6.37	104.99	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	1693	U	N1-C1'-C2'	6.34	122.25	114.00
34	b	1323	C	OP2-P-O3'	6.34	119.16	105.20
34	b	2129	C	N1-C1'-C2'	6.31	122.20	114.00
34	b	2750	A	O4'-C1'-N9	-6.30	103.16	108.20
34	b	254	G	N9-C1'-C2'	-6.29	105.08	112.00
34	b	2175	C	C4'-C3'-O3'	6.29	125.59	113.00
34	b	2607	G	P-O3'-C3'	6.28	127.24	119.70
23	W	36	C	OP1-P-O3'	-6.28	91.39	105.20
34	b	409	G	C2'-C3'-O3'	6.27	123.73	113.70
34	b	2066	C	N1-C1'-C2'	6.27	122.15	114.00
34	b	2593	U	N1-C1'-C2'	6.26	122.14	114.00
34	b	1272	A	O4'-C1'-N9	-6.25	103.20	108.20
34	b	1058	U	N3-C4-O4	-6.25	115.02	119.40
34	b	488	G	N9-C1'-C2'	-6.23	105.14	112.00
34	b	787	C	N1-C1'-C2'	6.22	122.09	114.00
34	b	1253	A	N9-C1'-C2'	6.20	122.06	114.00
34	b	2425	A	N9-C1'-C2'	6.18	122.04	114.00
34	b	2160	C	O4'-C1'-N1	6.17	113.14	108.20
34	b	72	U	N1-C1'-C2'	6.17	122.02	114.00
34	b	2496	C	O5'-P-OP2	-6.17	100.15	105.70
34	b	2324	U	C4'-C3'-O3'	6.17	125.33	113.00
34	b	2821	A	N9-C1'-C2'	6.15	121.99	114.00
34	b	2123	G	C1'-O4'-C4'	-6.14	104.98	109.90
34	b	250	G	N9-C1'-C2'	6.14	121.98	114.00
34	b	1758	U	N1-C1'-C2'	6.12	121.95	114.00
34	b	703	U	C2'-C3'-O3'	6.12	123.48	113.70
34	b	215	G	N9-C1'-C2'	6.11	121.94	114.00
34	b	618	G	N9-C1'-C2'	6.11	121.94	114.00
34	b	1801	A	N9-C1'-C2'	6.11	121.94	114.00
34	b	753	A	O3'-P-O5'	6.11	115.60	104.00
34	b	1055	G	C8-N9-C1'	-6.09	119.08	127.00
34	b	1323	C	O3'-P-O5'	-6.07	92.47	104.00
34	b	500	G	N9-C1'-C2'	-6.05	105.34	112.00
40	g	37	LEU	CB-CG-CD1	-6.05	100.72	111.00
34	b	1078	U	C2'-C3'-O3'	6.05	123.38	113.70
34	b	1349	C	C5'-C4'-O4'	6.05	116.36	109.10
34	b	91	A	N9-C1'-C2'	6.04	121.85	114.00
34	b	1059	G	N3-C4-N9	6.01	129.61	126.00
34	b	2225	A	N9-C1'-C2'	-6.01	105.39	112.00
34	b	450	G	C2'-C3'-O3'	5.99	123.29	113.70
34	b	1239	G	N9-C1'-C2'	-5.99	105.41	112.00
34	b	1824	G	N9-C1'-C2'	-5.98	105.42	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	196	A	O4'-C1'-N9	5.98	112.98	108.20
34	b	1055	G	C4-N9-C1'	5.97	134.27	126.50
34	b	1616	A	C5'-C4'-C3'	5.97	125.55	116.00
34	b	945	A	O5'-P-OP1	-5.96	100.34	105.70
34	b	1098	A	C4'-C3'-O3'	5.96	124.91	113.00
34	b	84	A	N9-C1'-C2'	-5.96	105.45	112.00
34	b	2131	U	N1-C2-N3	-5.94	111.33	114.90
34	b	126	A	N9-C1'-C2'	5.94	121.72	114.00
34	b	603	A	C2'-C3'-O3'	5.93	123.18	113.70
34	b	457	A	N9-C1'-C2'	5.91	121.68	114.00
34	b	1057	A	C4'-C3'-O3'	5.90	124.81	113.00
34	b	158	U	N1-C1'-C2'	5.89	121.66	114.00
34	b	372	G	C1'-O4'-C4'	-5.89	105.19	109.90
34	b	1779	U	C5'-C4'-O4'	5.89	116.17	109.10
34	b	729	G	O4'-C1'-N9	5.88	112.91	108.20
33	a	42	C	N1-C1'-C2'	5.87	121.63	114.00
34	b	2658	C	C2'-C3'-O3'	5.87	123.09	113.70
34	b	456	C	N1-C1'-C2'	5.86	121.62	114.00
34	b	1275	A	C1'-O4'-C4'	-5.86	105.21	109.90
34	b	1097	U	N1-C1'-C2'	-5.86	105.55	112.00
34	b	1211	C	O4'-C1'-N1	-5.86	103.51	108.20
34	b	1327	A	N9-C1'-C2'	5.86	121.61	114.00
34	b	574	A	O4'-C1'-N9	-5.85	103.52	108.20
34	b	1096	A	O4'-C1'-N9	5.85	112.88	108.20
34	b	2453	A	N9-C1'-C2'	-5.85	105.57	112.00
28	3	10	ARG	NE-CZ-NH2	5.84	123.22	120.30
34	b	2518	A	N9-C1'-C2'	5.84	121.59	114.00
34	b	2104	C	C2'-C3'-O3'	5.83	123.04	113.70
34	b	2576	G	P-O5'-C5'	5.83	130.23	120.90
34	b	458	G	O4'-C1'-N9	5.82	112.86	108.20
34	b	603	A	N9-C1'-C2'	5.82	121.57	114.00
34	b	1102	C	N1-C1'-C2'	5.81	121.56	114.00
34	b	2330	G	N9-C1'-C2'	-5.81	105.61	112.00
34	b	2133	G	N9-C1'-C2'	5.80	121.54	114.00
34	b	2056	G	N9-C1'-C2'	5.79	121.53	114.00
34	b	2273	A	N9-C1'-C2'	5.79	121.53	114.00
34	b	434	U	N1-C1'-C2'	-5.78	105.64	112.00
34	b	2340	A	C8-N9-C1'	-5.78	117.29	127.70
34	b	49	A	C4-N9-C1'	5.78	136.71	126.30
34	b	1618	A	N9-C1'-C2'	5.78	121.51	114.00
34	b	1060	U	C4'-C3'-O3'	5.77	124.55	113.00
34	b	2160	C	C1'-O4'-C4'	-5.77	105.28	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	2210	U	O4'-C1'-N1	-5.77	103.58	108.20
34	b	1522	A	N9-C1'-C2'	5.76	121.49	114.00
34	b	1349	C	N3-C4-N4	-5.76	113.97	118.00
34	b	1266	G	C1'-O4'-C4'	-5.76	105.30	109.90
34	b	1079	C	C3'-C2'-C1'	-5.75	96.90	101.50
34	b	2454	G	C4-N9-C1'	-5.75	119.03	126.50
34	b	1266	G	O4'-C1'-C2'	-5.74	100.06	105.80
34	b	2160	C	N1-C1'-C2'	-5.74	105.69	112.00
34	b	1509	A	N9-C1'-C2'	5.72	121.44	114.00
34	b	896	A	O4'-C1'-N9	5.72	112.77	108.20
34	b	979	A	C4'-C3'-C2'	-5.71	96.89	102.60
34	b	1382	G	N1-C2-N2	-5.71	111.06	116.20
34	b	1103	A	C2'-C3'-O3'	5.71	122.83	113.70
34	b	640	C	N1-C1'-C2'	5.70	121.41	114.00
34	b	2271	G	N9-C1'-C2'	5.69	121.39	114.00
34	b	24	G	N9-C1'-C2'	5.68	121.39	114.00
34	b	1211	C	C4'-C3'-O3'	-5.68	97.47	109.40
34	b	2333	A	N9-C1'-C2'	-5.68	105.75	112.00
34	b	1080	A	N1-C6-N6	-5.68	115.19	118.60
34	b	2161	C	C3'-C2'-C1'	-5.68	96.96	101.50
34	b	2160	C	C4'-C3'-C2'	-5.67	96.93	102.60
34	b	2732	G	O4'-C1'-N9	5.67	112.73	108.20
34	b	249	C	N1-C1'-C2'	-5.66	105.77	112.00
34	b	1693	U	O4'-C1'-N1	-5.65	103.68	108.20
34	b	1459	G	N9-C1'-C2'	5.64	121.34	114.00
34	b	31	C	N1-C1'-C2'	-5.63	105.80	112.00
1	A	1158	C	N3-C2-O2	-5.63	117.96	121.90
22	V	18	G	N9-C1'-C2'	5.62	121.31	114.00
34	b	160	A	N9-C1'-C2'	5.62	121.31	114.00
34	b	2045	C	N1-C1'-C2'	-5.62	105.82	112.00
34	b	251	A	N9-C1'-C2'	5.61	121.30	114.00
34	b	516	C	C2'-C3'-O3'	5.61	122.67	113.70
34	b	569	U	N1-C1'-C2'	5.61	121.29	114.00
1	A	365	U	C2-N1-C1'	5.60	124.42	117.70
34	b	447	A	N9-C1'-C2'	-5.60	105.84	112.00
34	b	1226	A	N9-C1'-C2'	5.60	121.28	114.00
34	b	834	G	C2'-C3'-O3'	5.59	122.65	113.70
34	b	801	G	C2'-C3'-O3'	5.58	122.62	113.70
34	b	2287	A	O4'-C1'-N9	5.57	112.65	108.20
34	b	2508	G	N9-C1'-C2'	-5.57	105.88	112.00
34	b	1349	C	O4'-C1'-C2'	-5.56	100.24	105.80
34	b	1265	A	N9-C1'-C2'	5.55	121.22	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	1069	A	O4'-C1'-N9	5.55	112.64	108.20
34	b	2282	G	O4'-C1'-N9	5.54	112.63	108.20
33	a	15	A	N9-C1'-C2'	5.54	121.20	114.00
47	o	25	ARG	NE-CZ-NH2	5.54	123.07	120.30
34	b	1585	C	N3-C4-C5	5.54	124.11	121.90
34	b	108	G	N9-C1'-C2'	-5.54	105.91	112.00
34	b	2330	G	C5'-C4'-O4'	5.53	115.74	109.10
34	b	783	A	O4'-C4'-C3'	-5.52	98.48	104.00
47	o	18	LEU	CB-CA-C	5.51	120.68	110.20
34	b	974	G	C1'-O4'-C4'	-5.51	105.49	109.90
34	b	1055	G	C5'-C4'-O4'	5.51	115.72	109.10
34	b	2055	C	C2'-C3'-O3'	5.51	122.52	113.70
34	b	2458	G	N9-C1'-C2'	-5.51	105.94	112.00
22	V	18	G	O4'-C1'-N9	-5.51	103.80	108.20
34	b	119	A	N9-C1'-C2'	5.50	121.15	114.00
34	b	1343	G	N9-C1'-C2'	5.50	121.15	114.00
34	b	2051	A	O5'-P-OP1	-5.50	100.75	105.70
34	b	62	U	O4'-C1'-N1	5.49	112.59	108.20
34	b	1607	C	O4'-C1'-N1	-5.49	103.81	108.20
34	b	241	A	O4'-C1'-N9	-5.49	103.81	108.20
34	b	1815	A	N9-C1'-C2'	5.48	121.12	114.00
34	b	835	C	N1-C1'-C2'	-5.48	105.97	112.00
34	b	2506	U	O3'-P-O5'	5.47	114.39	104.00
34	b	1156	A	N9-C1'-C2'	5.46	121.10	114.00
34	b	2750	A	N9-C1'-C2'	5.46	121.10	114.00
34	b	753	A	OP1-P-O3'	-5.46	93.19	105.20
34	b	1600	C	N1-C1'-C2'	5.46	121.09	114.00
34	b	1104	C	C5'-C4'-O4'	5.45	115.64	109.10
34	b	1755	A	N9-C1'-C2'	5.45	121.08	114.00
34	b	87	U	C2'-C3'-O3'	5.44	122.41	113.70
34	b	2057	G	N9-C1'-C2'	5.42	121.05	114.00
34	b	277	G	O4'-C1'-C2'	-5.41	100.39	105.80
34	b	1602	U	N1-C1'-C2'	-5.41	106.05	112.00
34	b	1667	G	O4'-C1'-C2'	-5.41	100.39	105.80
34	b	1761	C	N1-C1'-C2'	5.41	121.03	114.00
34	b	2034	U	N1-C1'-C2'	5.41	121.03	114.00
34	b	463	G	N9-C1'-C2'	-5.40	106.06	112.00
34	b	2471	A	N9-C1'-C2'	-5.40	106.06	112.00
1	A	1158	C	C6-N1-C1'	-5.38	114.34	120.80
34	b	2266	A	O4'-C1'-N9	-5.38	103.89	108.20
34	b	1079	C	C1'-O4'-C4'	-5.38	105.60	109.90
34	b	2340	A	C4-N9-C1'	5.37	135.96	126.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	399	U	C5'-C4'-C3'	5.37	124.59	116.00
34	b	621	A	N9-C1'-C2'	5.37	120.98	114.00
34	b	1762	A	C2'-C3'-O3'	5.36	122.28	113.70
34	b	1103	A	C5'-C4'-O4'	5.35	115.52	109.10
34	b	1667	G	C1'-C2'-O2'	5.34	126.63	110.60
34	b	465	G	N9-C1'-C2'	5.34	120.94	114.00
34	b	503	A	C5'-C4'-C3'	5.34	124.54	116.00
34	b	1425	G	N9-C1'-C2'	5.34	120.94	114.00
34	b	2288	A	C4'-C3'-O3'	5.34	123.68	113.00
34	b	1069	A	O4'-C4'-C3'	-5.34	98.66	104.00
34	b	1033	U	C3'-C2'-C1'	5.33	105.76	101.50
34	b	2010	G	N9-C1'-C2'	-5.32	106.14	112.00
34	b	2161	C	P-O5'-C5'	5.32	129.41	120.90
34	b	387	U	N1-C1'-C2'	5.32	120.91	114.00
34	b	1814	G	N9-C1'-C2'	5.32	120.91	114.00
34	b	1100	C	C4'-C3'-O3'	5.31	123.62	113.00
34	b	49	A	C3'-C2'-C1'	-5.31	97.25	101.50
34	b	2175	C	C4'-C3'-C2'	-5.31	97.29	102.60
34	b	33	C	N1-C1'-C2'	-5.31	106.16	112.00
34	b	571	U	O4'-C1'-N1	5.30	112.44	108.20
34	b	1585	C	C6-N1-C2	5.30	122.42	120.30
34	b	859	G	O4'-C1'-N9	5.29	112.44	108.20
34	b	2564	A	N9-C1'-C2'	5.29	120.88	114.00
34	b	281	C	N1-C1'-C2'	5.29	120.88	114.00
34	b	1427	A	N9-C1'-C2'	5.28	120.86	114.00
34	b	1461	C	N1-C1'-C2'	5.27	120.85	114.00
34	b	2732	G	O4'-C1'-C2'	-5.27	100.53	105.80
34	b	2422	C	O4'-C1'-N1	5.26	112.41	108.20
34	b	1133	A	C1'-O4'-C4'	-5.26	105.69	109.90
34	b	1086	A	N9-C1'-C2'	5.25	120.83	114.00
34	b	896	A	C1'-O4'-C4'	-5.25	105.70	109.90
34	b	896	A	O4'-C4'-C3'	-5.24	98.76	104.00
34	b	446	G	C3'-C2'-C1'	5.23	105.68	101.50
52	t	3	ARG	NE-CZ-NH1	5.23	122.91	120.30
25	0	57	ARG	NE-CZ-NH2	5.22	122.91	120.30
34	b	1616	A	N9-C1'-C2'	5.21	120.77	114.00
34	b	783	A	C2'-C3'-O3'	5.21	122.03	113.70
34	b	2168	G	C4'-C3'-O3'	5.21	123.41	113.00
34	b	1055	G	C3'-C2'-C1'	5.20	105.66	101.50
34	b	1388	G	C2'-C3'-O3'	5.20	122.02	113.70
34	b	2282	G	O4'-C1'-C2'	-5.20	100.60	105.80
34	b	2590	A	N9-C1'-C2'	-5.20	106.28	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	2391	G	C1'-O4'-C4'	-5.19	105.75	109.90
34	b	2518	A	C5'-C4'-O4'	5.19	115.33	109.10
34	b	2422	C	C1'-O4'-C4'	-5.17	105.76	109.90
34	b	1253	A	O4'-C1'-N9	-5.17	104.07	108.20
37	d	4	LEU	CB-CG-CD1	5.17	119.78	111.00
34	b	979	A	C5'-C4'-O4'	5.15	115.28	109.10
34	b	2798	U	N1-C1'-C2'	5.14	120.69	114.00
34	b	1059	G	N3-C4-C5	-5.14	126.03	128.60
34	b	1287	A	N9-C1'-C2'	5.14	120.68	114.00
34	b	1772	A	C2'-C3'-O3'	5.13	121.90	113.70
34	b	2471	A	C4'-C3'-O3'	5.13	123.25	113.00
34	b	957	C	N1-C1'-C2'	5.12	120.66	114.00
34	b	1377	G	N9-C1'-C2'	5.12	120.66	114.00
34	b	1802	A	N9-C1'-C2'	5.12	120.66	114.00
23	W	49	G	C2'-C3'-O3'	5.12	121.89	113.70
34	b	1141	U	N1-C1'-C2'	5.11	120.65	114.00
34	b	242	G	O4'-C1'-N9	5.11	112.29	108.20
34	b	100	U	C1'-O4'-C4'	-5.09	105.83	109.90
34	b	974	G	O4'-C1'-C2'	-5.09	100.71	105.80
34	b	253	C	N1-C1'-C2'	-5.08	106.42	112.00
33	a	66	A	C2'-C3'-O3'	5.07	121.81	113.70
41	h	66	ASN	N-CA-C	5.07	124.69	111.00
34	b	1009	A	N9-C1'-C2'	5.07	120.59	114.00
34	b	2330	G	C4'-C3'-C2'	-5.07	97.53	102.60
34	b	250	G	O4'-C1'-N9	-5.07	104.15	108.20
22	V	18	G	O4'-C4'-C3'	-5.06	98.94	104.00
34	b	1698	A	O4'-C1'-N9	-5.06	104.15	108.20
34	b	2288	A	O4'-C1'-N9	5.06	112.25	108.20
34	b	584	C	O4'-C1'-C2'	-5.06	100.74	105.80
38	e	59	PRO	C-N-CA	5.06	134.34	121.70
34	b	196	A	C1'-O4'-C4'	-5.05	105.86	109.90
1	A	188	C	N3-C2-O2	-5.05	118.36	121.90
34	b	1204	A	O4'-C1'-N9	-5.05	104.16	108.20
34	b	801	G	N9-C1'-C2'	5.03	120.54	114.00
34	b	1266	G	N9-C1'-C2'	-5.03	106.47	112.00
34	b	2497	A	N9-C1'-C2'	-5.03	106.47	112.00
34	b	779	U	C5'-C4'-O4'	5.03	115.14	109.10
34	b	1599	U	N1-C1'-C2'	5.03	120.54	114.00
34	b	783	A	C4'-C3'-O3'	5.03	123.06	113.00
34	b	1143	A	N9-C1'-C2'	5.03	120.53	114.00
34	b	2488	G	N9-C1'-C2'	5.03	120.53	114.00
34	b	1037	G	C5'-C4'-C3'	5.03	124.04	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	b	1355	G	N9-C1'-C2'	-5.03	106.47	112.00
34	b	195	A	N9-C1'-C2'	-5.02	106.48	112.00
34	b	759	G	C2'-C3'-O3'	5.02	121.73	113.70
34	b	62	U	C1'-O4'-C4'	-5.02	105.89	109.90
34	b	1913	A	C2'-C3'-O3'	5.02	121.73	113.70
34	b	176	A	N9-C1'-C2'	5.01	120.51	114.00
34	b	654	A	C2'-C3'-O3'	5.01	121.71	113.70
34	b	1607	C	N1-C1'-C2'	5.01	120.51	114.00
34	b	2175	C	O4'-C4'-C3'	-5.01	98.99	104.00
34	b	1069	A	C4'-C3'-O3'	5.00	123.00	113.00
34	b	1101	U	N1-C1'-C2'	-5.00	106.50	112.00

There are no chirality outliers.

All (71) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
27	2	3	LYS	Peptide
9	I	124	PRO	Peptide
34	b	1057	A	Sidechain
34	b	1059	G	Sidechain
34	b	1079	C	Sidechain
34	b	1080	A	Sidechain
34	b	1096	A	Sidechain
34	b	1097	U	Sidechain
34	b	119	A	Sidechain
34	b	1204	A	Sidechain
34	b	1225	G	Sidechain
34	b	1238	G	Sidechain
34	b	1253	A	Sidechain
34	b	1266	G	Sidechain
34	b	1272	A	Sidechain
34	b	1275	A	Sidechain
34	b	1300	G	Sidechain
34	b	1349	C	Sidechain
34	b	1382	G	Sidechain
34	b	1392	A	Sidechain
34	b	1667	G	Sidechain
34	b	1693	U	Sidechain
34	b	1698	A	Sidechain
34	b	1759	A	Sidechain
34	b	1773	A	Sidechain
34	b	1774	C	Sidechain

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Mol	Chain	Res	Type	Group
34	b	1775	U	Sidechain
34	b	1829	A	Sidechain
34	b	1943	U	Sidechain
34	b	195	A	Sidechain
34	b	1967	C	Sidechain
34	b	2032	G	Sidechain
34	b	2092	U	Sidechain
34	b	2123	G	Sidechain
34	b	2266	A	Sidechain
34	b	2330	G	Sidechain
34	b	241	A	Sidechain
34	b	242	G	Sidechain
34	b	2449	U	Sidechain
34	b	2453	A	Sidechain
34	b	2454	G	Sidechain
34	b	246	C	Sidechain
34	b	25	U	Sidechain
34	b	250	G	Sidechain
34	b	2518	A	Sidechain
34	b	2564	A	Sidechain
34	b	2589	A	Sidechain
34	b	2590	A	Sidechain
34	b	2597	G	Sidechain
34	b	372	G	Sidechain
34	b	388	G	Sidechain
34	b	446	G	Sidechain
34	b	450	G	Sidechain
34	b	464	U	Sidechain
34	b	500	G	Sidechain
34	b	603	A	Sidechain
34	b	674	G	Sidechain
34	b	779	U	Sidechain
34	b	782	A	Sidechain
34	b	783	A	Sidechain
34	b	801	G	Sidechain
34	b	805	G	Sidechain
34	b	959	A	Sidechain
34	b	973	A	Sidechain
34	b	979	A	Sidechain
34	b	986	C	Sidechain
35	c	232	HIS	Peptide
37	d	151	THR	Peptide

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Mol	Chain	Res	Type	Group
43	k	34	GLY	Peptide
44	l	102	GLY	Peptide
50	r	50	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32831	0	16518	776	0
2	B	1704	0	1732	54	0
3	C	1624	0	1699	62	0
4	D	1643	0	1710	92	0
5	E	1105	0	1148	43	0
6	F	817	0	808	29	0
7	G	1174	0	1230	37	0
8	H	979	0	1034	35	0
9	I	1022	0	1070	112	0
10	J	786	0	828	44	0
11	K	877	0	887	54	0
12	L	955	0	1019	30	0
13	M	876	0	936	39	0
14	N	774	0	827	38	0
15	O	716	0	742	21	0
16	P	649	0	664	121	0
17	Q	648	0	691	23	0
18	R	455	0	478	13	0
19	S	637	0	665	32	0
20	T	665	0	714	22	0
21	U	425	0	449	60	0
22	V	1620	0	817	145	0
23	W	1599	0	813	29	0
24	X	231	0	120	32	0
25	0	625	0	652	4	0
26	1	501	0	531	3	0
27	2	449	0	488	8	0
28	3	444	0	458	12	0
29	4	409	0	440	2	0
30	6	377	0	418	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	7	504	0	572	2	0
32	8	302	0	343	5	0
33	a	2506	0	1270	0	0
34	b	62321	0	31311	0	0
35	c	2082	0	2154	0	0
36	i	976	0	1008	0	0
37	d	1565	0	1616	0	0
38	e	1552	0	1619	0	0
39	f	1410	0	1444	0	0
40	g	1323	0	1371	0	0
41	h	1111	0	1148	0	0
42	j	1129	0	1162	0	0
43	k	938	0	1012	0	0
44	l	1053	0	1129	0	0
45	m	1063	0	1143	0	0
46	n	960	0	1000	0	0
47	o	892	0	923	0	0
48	p	917	0	961	0	0
49	q	947	0	1019	0	0
50	r	816	0	839	0	0
51	s	857	0	922	0	0
52	t	738	0	807	0	0
53	u	779	0	831	0	0
54	w	753	0	780	0	0
55	y	569	0	581	0	0
56	z	211	0	206	0	0
57	b	20	0	11	0	0
All	All	145911	0	97768	1662	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (1662) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:G:H21	16:P:13:LYS:NZ	1.05	1.47
21:U:27:VAL:O	21:U:31:VAL:CG1	1.65	1.43
1:A:392:C:C5'	16:P:12:LYS:HD2	1.47	1.41
1:A:375:U:H5'	16:P:6:LEU:CD2	1.50	1.39
9:I:112:ARG:NH2	9:I:114:LYS:HD2	1.39	1.36
1:A:450:G:N2	16:P:13:LYS:NZ	1.72	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:27:VAL:O	21:U:31:VAL:HG11	1.15	1.32
1:A:1348:U:OP2	9:I:111:GLU:HG2	1.21	1.29
9:I:112:ARG:NH1	9:I:114:LYS:HG2	1.47	1.28
1:A:392:C:O5'	16:P:12:LYS:HD2	1.31	1.26
1:A:1348:U:P	9:I:111:GLU:HG2	1.74	1.26
1:A:1338:G:C8	23:W:41:C:O2'	1.90	1.25
9:I:112:ARG:NH1	9:I:114:LYS:CG	1.99	1.25
1:A:722:G:OP2	21:U:44:ARG:NH1	1.68	1.23
28:3:29:SER:OG	28:3:40:ARG:HD2	1.37	1.20
1:A:1348:U:O5'	9:I:111:GLU:CD	1.78	1.20
9:I:112:ARG:HH12	9:I:114:LYS:CG	1.54	1.20
1:A:392:C:OP1	16:P:12:LYS:CG	1.93	1.17
22:V:37:A:C2'	22:V:38:A:H5''	1.73	1.17
24:X:20:C:HO2'	24:X:21:A:C4'	1.58	1.16
22:V:33:U:O2'	22:V:34:A:H2	1.24	1.16
21:U:27:VAL:C	21:U:31:VAL:HG11	1.66	1.14
1:A:1338:G:H8	23:W:41:C:O2'	1.24	1.14
22:V:38:A:H2'	22:V:39:U:C6	1.82	1.13
22:V:33:U:O2'	22:V:34:A:C2	1.97	1.12
21:U:27:VAL:C	21:U:31:VAL:CG1	2.15	1.12
1:A:375:U:H5'	16:P:6:LEU:HD23	1.16	1.11
1:A:375:U:H5'	16:P:6:LEU:HD22	1.29	1.10
1:A:1350:A:OP2	9:I:119:LYS:NZ	1.83	1.10
22:V:37:A:H2'	22:V:38:A:C5'	1.80	1.10
1:A:624:C:O2'	16:P:10:GLY:O	1.69	1.10
1:A:230:G:H5''	16:P:31:ARG:HH21	1.07	1.09
1:A:402:G:OP2	4:D:69:ARG:NH1	1.85	1.09
1:A:392:C:H5'	16:P:12:LYS:HD2	1.24	1.09
1:A:255:G:OP1	17:Q:70:LYS:NZ	1.86	1.08
1:A:427:U:OP2	4:D:32:LYS:NZ	1.87	1.07
25:0:68:LEU:HD23	25:0:71:LEU:HD12	1.37	1.07
1:A:375:U:C5'	16:P:6:LEU:HD23	1.82	1.07
1:A:392:C:P	16:P:12:LYS:CD	2.44	1.06
8:H:4:ASP:OD1	8:H:76:ARG:NH1	1.88	1.06
24:X:20:C:O2'	24:X:21:A:O4'	1.72	1.06
2:B:72:LYS:NZ	2:B:164:ASP:OD2	1.90	1.05
28:3:29:SER:OG	28:3:40:ARG:CD	2.04	1.04
24:X:20:C:O2'	24:X:21:A:C4'	2.04	1.03
1:A:392:C:OP1	16:P:12:LYS:CD	2.05	1.03
1:A:230:G:H5''	16:P:31:ARG:NH2	1.73	1.03
21:U:27:VAL:HG13	21:U:31:VAL:CG2	1.86	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:C:OP1	16:P:12:LYS:CB	2.07	1.02
1:A:392:C:H5'	16:P:12:LYS:CD	1.90	1.01
1:A:392:C:C5'	16:P:12:LYS:CD	2.38	1.01
1:A:1379:G:O6	7:G:2:ARG:NH1	1.91	1.01
21:U:27:VAL:HG13	21:U:31:VAL:HG21	1.03	1.01
1:A:693:G:OP1	11:K:126:ARG:NH1	1.92	1.00
9:I:112:ARG:HH12	9:I:114:LYS:HG2	0.88	1.00
24:X:19:U:O2	24:X:20:C:N4	1.94	1.00
1:A:1348:U:O5'	9:I:111:GLU:OE2	1.80	1.00
10:J:63:ASP:OD1	14:N:97:LYS:NZ	1.95	0.99
6:F:2:ARG:HH11	6:F:68:GLN:HE21	1.10	0.98
1:A:1348:U:OP2	9:I:111:GLU:CG	2.09	0.98
1:A:1340:A:O2'	23:W:31:C:O2'	1.80	0.98
1:A:1348:U:P	9:I:111:GLU:CG	2.52	0.97
1:A:261:U:OP2	20:T:73:ARG:NH2	1.98	0.97
1:A:1054:C:N4	22:V:34:A:C8	2.34	0.96
1:A:392:C:OP1	16:P:12:LYS:HB2	1.65	0.96
9:I:105:ARG:NH1	9:I:106:ASP:O	1.98	0.96
9:I:112:ARG:HH22	9:I:114:LYS:HD2	1.02	0.95
9:I:112:ARG:CZ	9:I:114:LYS:HD2	1.94	0.95
1:A:392:C:O5'	16:P:12:LYS:CD	2.14	0.95
32:8:3:VAL:HG21	32:8:36:ARG:NH1	1.82	0.94
21:U:25:ALA:O	21:U:27:VAL:N	2.00	0.94
7:G:52:ARG:NH1	7:G:124:SER:OG	2.00	0.94
21:U:29:ALA:O	21:U:31:VAL:N	1.99	0.94
22:V:37:A:H2'	22:V:38:A:H5''	0.94	0.93
1:A:1228:C:OP1	13:M:106:ARG:NH1	2.01	0.93
21:U:27:VAL:CG1	21:U:31:VAL:HG21	1.97	0.93
11:K:116:PRO:HD2	21:U:27:VAL:HG21	1.51	0.93
1:A:450:G:N2	16:P:13:LYS:HZ2	1.46	0.93
1:A:362:G:N2	1:A:365:U:OP2	2.02	0.92
6:F:2:ARG:NH1	6:F:68:GLN:HE21	1.66	0.92
28:3:29:SER:HG	28:3:40:ARG:HD2	1.33	0.92
1:A:104:G:OP2	20:T:12:GLN:NE2	2.03	0.92
9:I:118:ARG:HG2	9:I:124:PRO:HD3	1.50	0.92
14:N:63:CYS:HG	14:N:79:SER:HG	1.15	0.91
1:A:375:U:C5'	16:P:6:LEU:CD2	2.42	0.91
1:A:392:C:OP1	16:P:12:LYS:HD3	1.68	0.91
21:U:27:VAL:CG1	21:U:31:VAL:HG11	2.00	0.91
11:K:16:SER:OG	11:K:79:LYS:NZ	2.03	0.90
21:U:27:VAL:C	21:U:31:VAL:HG12	1.89	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:27:VAL:CA	21:U:31:VAL:HG11	2.02	0.90
1:A:1173:U:OP1	7:G:4:ARG:NH1	2.04	0.90
1:A:1231:G:OP1	9:I:128:LYS:NZ	2.05	0.89
9:I:112:ARG:HH22	9:I:114:LYS:CD	1.84	0.89
1:A:575:G:O2'	1:A:821:G:OP2	1.90	0.89
27:2:5:ILE:CD1	27:2:40:ASP:OD1	2.21	0.88
22:V:75:C:O2'	22:V:76:A:O4'	1.90	0.88
1:A:450:G:N2	16:P:13:LYS:HZ3	1.50	0.88
1:A:82:G:N2	1:A:88:U:OP1	2.07	0.88
10:J:9:ARG:HH11	10:J:71:LEU:HD21	1.37	0.88
1:A:1013:G:N2	1:A:1016:A:OP2	2.07	0.88
1:A:1054:C:N3	22:V:34:A:C8	2.42	0.87
24:X:19:U:H6	24:X:19:U:H5'	1.40	0.87
21:U:27:VAL:HA	21:U:31:VAL:HB	1.55	0.87
1:A:1266:G:N2	1:A:1269:A:OP2	2.06	0.87
6:F:38:ARG:NH1	6:F:97:THR:O	2.08	0.87
1:A:842:U:O2'	1:A:844:G:OP2	1.93	0.86
21:U:27:VAL:CA	21:U:31:VAL:CG1	2.54	0.86
4:D:182:LYS:NZ	4:D:183:ARG:NH1	2.24	0.86
1:A:522:C:OP2	12:L:65:TYR:OH	1.94	0.86
8:H:6:ILE:HB	8:H:76:ARG:NH1	1.90	0.85
24:X:20:C:HO2'	24:X:21:A:C1'	1.89	0.85
1:A:392:C:P	16:P:12:LYS:HD3	2.15	0.85
1:A:1305:G:N2	1:A:1332:A:OP2	2.08	0.85
1:A:1054:C:N4	22:V:34:A:N7	2.25	0.84
1:A:392:C:P	16:P:12:LYS:HD2	2.13	0.84
16:P:28:ARG:HE	16:P:29:ASN:HD21	1.23	0.84
22:V:75:C:O2'	22:V:76:A:OP1	1.95	0.84
1:A:1367:C:H5'	10:J:62:ARG:NH1	1.93	0.83
22:V:56:C:H2'	22:V:56:C:O2	1.76	0.83
1:A:1178:G:N7	9:I:98:ARG:NH1	2.27	0.83
13:M:28:ARG:HH21	13:M:62:PHE:HB2	1.41	0.83
1:A:1032:G:N2	1:A:1032:G:OP2	2.11	0.82
1:A:826:C:O2	8:H:15:ASN:ND2	2.13	0.82
1:A:230:G:C5'	16:P:31:ARG:HH21	1.92	0.82
1:A:1350:A:OP1	9:I:122:ARG:NH1	2.12	0.82
21:U:27:VAL:O	21:U:31:VAL:HG12	1.77	0.82
9:I:21:LYS:HB2	9:I:61:ASP:HB2	1.62	0.82
1:A:1338:G:H8	23:W:41:C:HO2'	0.85	0.82
24:X:20:C:O2'	24:X:21:A:H4'	1.77	0.82
7:G:110:ARG:HD2	7:G:118:ARG:HA	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1441:A:H61	1:A:1462:C:H1'	1.46	0.81
1:A:177:G:N2	1:A:177:G:OP2	2.12	0.81
24:X:12:C:H4'	24:X:13:U:OP1	1.80	0.81
15:O:73:ASP:OD2	15:O:76:ARG:N	2.14	0.81
1:A:203:G:N1	1:A:214:C:N3	2.29	0.81
1:A:321:A:H61	1:A:332:G:H1	1.26	0.81
1:A:1054:C:C4	22:V:34:A:C8	2.70	0.80
24:X:12:C:OP2	24:X:12:C:H3'	1.80	0.80
27:2:5:ILE:HD11	27:2:40:ASP:OD1	1.79	0.80
1:A:1052:U:O2'	1:A:1055:A:OP2	1.97	0.80
11:K:126:ARG:HG2	11:K:128:VAL:H	1.46	0.80
16:P:28:ARG:NE	16:P:29:ASN:HD21	1.79	0.80
1:A:460:A:N6	1:A:471:U:O4	2.13	0.79
4:D:10:LEU:HD13	4:D:62:ARG:HD2	1.63	0.79
1:A:230:G:O3'	16:P:31:ARG:NH2	2.14	0.79
22:V:38:A:H2'	22:V:39:U:H6	1.43	0.79
1:A:376:G:OP1	16:P:5:ARG:HB2	1.81	0.79
24:X:12:C:C4'	24:X:13:U:OP1	2.30	0.79
22:V:56:C:O2	22:V:57:G:C5	2.35	0.79
22:V:18:G:O2'	22:V:19:G:C5	2.36	0.79
21:U:25:ALA:HA	21:U:29:ALA:HB3	1.65	0.79
1:A:944:G:N2	1:A:1339:A:OP2	2.15	0.78
1:A:1348:U:C5'	9:I:111:GLU:CD	2.51	0.78
22:V:33:U:C2'	22:V:34:A:H2	1.96	0.78
24:X:20:C:O2'	24:X:21:A:C1'	2.30	0.78
22:V:56:C:O2	22:V:57:G:C4	2.36	0.78
9:I:112:ARG:NH2	9:I:114:LYS:CD	2.35	0.78
21:U:27:VAL:HG12	21:U:31:VAL:HG11	1.65	0.78
5:E:84:VAL:HG11	5:E:142:GLY:HA3	1.65	0.78
22:V:40:C:O2'	22:V:41:C:O5'	2.02	0.78
1:A:136:C:C4'	16:P:1:MET:HG3	2.14	0.78
1:A:392:C:H5'	16:P:12:LYS:CE	2.13	0.78
14:N:80:ARG:HE	14:N:81:ILE:HG23	1.49	0.77
22:V:27:G:N2	22:V:28:G:C5	2.53	0.77
24:X:18:C:C6	24:X:18:C:H5''	2.19	0.77
1:A:1118:U:OP2	9:I:105:ARG:NE	2.19	0.77
1:A:1348:U:H5''	9:I:111:GLU:OE1	1.85	0.77
9:I:112:ARG:NH1	9:I:114:LYS:HG3	1.99	0.77
12:L:78:VAL:N	12:L:102:ASP:OD2	2.17	0.77
1:A:184:G:H5''	1:A:224:U:H4'	1.68	0.76
1:A:392:C:OP1	16:P:12:LYS:HG3	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:C:H5'	16:P:12:LYS:HE3	1.67	0.76
32:8:3:VAL:HG21	32:8:36:ARG:HH12	1.50	0.76
1:A:18:C:OP1	5:E:131:ASN:ND2	2.19	0.76
16:P:22:ALA:HA	16:P:33:ILE:HG13	1.65	0.76
1:A:1027:C:N3	1:A:1034:G:N2	2.33	0.76
9:I:83:THR:HG21	9:I:102:PHE:HB3	1.67	0.76
11:K:51:PHE:HA	11:K:55:ARG:NH1	2.00	0.76
26:1:3:ALA:O	26:1:7:ARG:HG3	1.85	0.76
1:A:1307:U:OP1	13:M:99:GLN:NE2	2.19	0.76
1:A:445:G:H1	1:A:489:C:H42	1.33	0.75
10:J:9:ARG:HB3	10:J:71:LEU:HD11	1.68	0.75
1:A:231:U:P	16:P:31:ARG:HH22	2.10	0.75
1:A:5:U:H4'	1:A:6:G:H5'	1.68	0.75
15:O:87:ARG:O	15:O:88:ARG:NH1	2.19	0.75
21:U:27:VAL:HA	21:U:31:VAL:CG1	2.16	0.75
6:F:91:ARG:HG3	6:F:92:THR:HG23	1.68	0.75
21:U:27:VAL:HA	21:U:31:VAL:CB	2.17	0.75
1:A:796:C:H5''	11:K:126:ARG:HG3	1.69	0.74
9:I:56:MET:HG2	9:I:57:VAL:HG23	1.70	0.74
3:C:160:GLU:HG3	3:C:161:ILE:HG12	1.67	0.74
7:G:137:ARG:HH11	7:G:141:HIS:CE1	2.03	0.74
1:A:136:C:O4'	16:P:1:MET:HG3	1.86	0.74
3:C:69:THR:H	3:C:103:ALA:HB1	1.52	0.74
4:D:152:SER:HA	4:D:155:LYS:NZ	2.02	0.74
12:L:53:ARG:HH21	12:L:61:GLU:HG2	1.53	0.73
1:A:375:U:H1'	16:P:17:TYR:HE2	1.53	0.73
27:2:5:ILE:HD11	27:2:45:ARG:NH1	2.04	0.73
1:A:942:G:N2	9:I:126:PHE:O	2.21	0.73
9:I:112:ARG:NH1	9:I:114:LYS:CD	2.51	0.73
22:V:37:A:C2'	22:V:38:A:C5'	2.53	0.73
21:U:29:ALA:C	21:U:31:VAL:H	1.92	0.73
1:A:81:A:N6	1:A:87:C:O2'	2.22	0.72
8:H:91:LEU:HD12	8:H:92:PRO:HD2	1.70	0.72
8:H:95:MET:HB2	8:H:129:ALA:HB1	1.71	0.72
22:V:73:A:N3	22:V:73:A:H2'	2.04	0.72
1:A:1350:A:P	9:I:122:ARG:HH11	2.12	0.72
4:D:141:VAL:HG13	4:D:178:GLU:HG3	1.71	0.72
22:V:38:A:O2'	22:V:39:U:O4'	2.06	0.72
1:A:1058:G:H1	1:A:1199:U:H3	1.36	0.72
1:A:1038:C:H2'	1:A:1039:G:H8	1.54	0.72
3:C:129:PHE:HB3	3:C:156:LEU:HD23	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:188:ALA:HB3	3:C:195:ILE:HB	1.70	0.72
17:Q:57:VAL:HG23	17:Q:78:VAL:HB	1.72	0.72
1:A:1130:A:N6	1:A:1144:G:N3	2.36	0.72
1:A:927:G:O2'	1:A:1503:A:N7	2.21	0.72
1:A:976:G:H1	1:A:1362:A:HO2'	1.29	0.72
14:N:22:LYS:HE2	14:N:23:ARG:NH1	2.05	0.72
4:D:182:LYS:HZ2	4:D:183:ARG:NH1	1.86	0.72
6:F:6:ILE:HB	6:F:62:MET:HB2	1.71	0.72
1:A:1164:G:N2	1:A:1172:C:N3	2.36	0.71
2:B:185:ILE:HG22	2:B:199:ILE:HB	1.71	0.71
2:B:28:PRO:O	2:B:44:LYS:NZ	2.23	0.71
22:V:39:U:O2'	22:V:40:C:H5'	1.89	0.71
22:V:56:C:O2	22:V:56:C:C2'	2.37	0.71
1:A:1131:G:H22	1:A:1144:G:H4'	1.55	0.71
5:E:80:LEU:HG	5:E:82:HIS:H	1.55	0.71
1:A:301:G:H2'	1:A:302:G:H8	1.54	0.71
8:H:12:ARG:HH12	8:H:27:PRO:HD2	1.56	0.71
1:A:974:A:OP2	14:N:68:ARG:NH2	2.23	0.71
1:A:107:G:O6	20:T:9:ARG:NH1	2.24	0.71
22:V:40:C:H2'	22:V:41:C:H6	1.56	0.71
8:H:10:LEU:HD22	8:H:74:ILE:HD11	1.71	0.71
9:I:40:ARG:HA	9:I:44:ARG:HD2	1.72	0.71
16:P:51:ARG:NH2	16:P:53:ASP:HB2	2.06	0.70
1:A:1341:U:H2'	9:I:126:PHE:HB2	1.73	0.70
9:I:129:ARG:HA	23:W:32:A:OP1	1.91	0.70
1:A:1367:C:OP2	9:I:117:LEU:HB2	1.92	0.70
1:A:227:G:O2'	16:P:63:GLN:HG3	1.92	0.70
1:A:327:A:H1'	1:A:329:A:H1'	1.72	0.70
1:A:1342:C:H5'	9:I:126:PHE:HA	1.73	0.70
1:A:106:C:O2'	1:A:379:C:OP1	2.09	0.70
9:I:112:ARG:HH12	9:I:114:LYS:CD	2.04	0.70
9:I:112:ARG:CZ	9:I:114:LYS:CD	2.69	0.70
1:A:178:C:OP2	20:T:59:ARG:NH2	2.20	0.70
1:A:442:G:O6	1:A:492:C:N4	2.19	0.70
22:V:30:G:N1	22:V:40:C:N4	2.40	0.70
1:A:1379:G:N7	7:G:2:ARG:NH2	2.40	0.70
1:A:979:C:O2'	14:N:52:ARG:NH2	2.25	0.70
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.73	0.70
1:A:228:A:HO2'	16:P:60:TRP:HZ3	1.37	0.70
24:X:19:U:C5'	24:X:19:U:H6	2.04	0.69
1:A:264:C:H4'	17:Q:64:ARG:HH21	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:72:G:H3'	23:W:73:A:H5'	1.72	0.69
4:D:58:GLN:HG3	4:D:62:ARG:NH1	2.08	0.69
1:A:1117:A:N6	1:A:1184:G:O6	2.25	0.69
10:J:5:ARG:N	10:J:76:ILE:O	2.25	0.69
19:S:25:GLY:O	19:S:27:LYS:NZ	2.24	0.69
3:C:57:GLU:HB3	3:C:64:ARG:HB2	1.73	0.69
21:U:24:LYS:O	21:U:28:LEU:HB2	1.92	0.69
16:P:73:ALA:O	16:P:77:GLU:HB2	1.93	0.69
27:2:5:ILE:HD12	27:2:40:ASP:OD1	1.92	0.69
13:M:22:TYR:O	13:M:69:ARG:NH2	2.26	0.69
1:A:1308:U:H2'	1:A:1309:G:H8	1.58	0.69
1:A:1054:C:N4	22:V:34:A:C5	2.60	0.69
11:K:22:ILE:HG23	11:K:85:VAL:HA	1.75	0.69
24:X:18:C:H2'	24:X:19:U:H5''	1.74	0.69
1:A:1267:C:N3	1:A:1327:C:O2'	2.25	0.68
1:A:8:A:N6	4:D:201:GLU:O	2.26	0.68
4:D:10:LEU:HB3	4:D:62:ARG:HE	1.57	0.68
1:A:1348:U:P	9:I:111:GLU:CD	2.71	0.68
1:A:580:C:H5''	15:O:57:ARG:NH1	2.08	0.68
6:F:12:PRO:O	6:F:44:ARG:NH2	2.26	0.68
1:A:1129:C:H42	1:A:1143:G:H1	1.42	0.68
1:A:710:G:OP1	6:F:53:LYS:NZ	2.26	0.68
6:F:98:GLU:HG3	6:F:100:SER:H	1.58	0.68
4:D:73:ASN:HA	4:D:76:LYS:HE2	1.74	0.68
1:A:790:A:OP1	23:W:38:U:O2'	2.07	0.68
1:A:1348:U:C5'	9:I:111:GLU:OE1	2.42	0.68
20:T:50:PHE:HA	20:T:53:MET:HG2	1.74	0.68
1:A:1302:C:H1'	13:M:16:ILE:HG13	1.76	0.68
22:V:70:G:C2	22:V:71:G:C8	2.81	0.68
19:S:50:VAL:HG11	19:S:70:LEU:HB3	1.76	0.68
11:K:51:PHE:HA	11:K:55:ARG:HH12	1.56	0.68
28:3:27:SER:O	28:3:40:ARG:HG2	1.93	0.67
22:V:37:A:C3'	22:V:38:A:C5'	2.71	0.67
22:V:19:G:N2	22:V:57:G:N2	2.42	0.67
9:I:5:TYR:HB2	9:I:20:ILE:HB	1.74	0.67
1:A:1065:U:H1'	1:A:1066:C:OP2	1.93	0.67
1:A:147:G:H2'	1:A:148:G:C8	2.29	0.67
16:P:59:HIS:CE1	16:P:63:GLN:HE22	2.13	0.67
22:V:18:G:O2'	22:V:19:G:C6	2.47	0.67
32:8:3:VAL:HG22	32:8:36:ARG:HB3	1.77	0.67
5:E:64:GLU:OE1	5:E:67:ARG:NH2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:128:GLU:HB2	7:G:130:LYS:HZ3	1.60	0.67
4:D:123:MET:N	4:D:143:SER:O	2.26	0.66
1:A:700:G:H5'	1:A:701:U:OP2	1.93	0.66
1:A:374:A:H4'	1:A:452:A:H1'	1.77	0.66
1:A:820:U:H4'	1:A:821:G:OP2	1.93	0.66
4:D:131:ILE:HG22	4:D:133:SER:H	1.61	0.66
1:A:1193:G:O6	3:C:2:GLN:NE2	2.17	0.66
3:C:76:ILE:HG13	3:C:80:GLY:HA2	1.77	0.66
2:B:25:LYS:HD2	2:B:191:ASP:OD2	1.95	0.66
6:F:2:ARG:HH11	6:F:68:GLN:NE2	1.87	0.66
24:X:17:C:OP2	24:X:17:C:H6	1.78	0.66
1:A:230:G:C5'	16:P:31:ARG:NH2	2.55	0.66
1:A:720:C:H5''	1:A:721:G:OP2	1.96	0.66
14:N:52:ARG:HG2	14:N:58:ARG:NH1	2.11	0.66
1:A:184:G:O2'	1:A:185:U:O5'	2.13	0.66
20:T:79:THR:HA	20:T:82:ILE:HG12	1.76	0.66
1:A:1134:G:H1	1:A:1140:C:H42	1.42	0.66
3:C:51:VAL:HA	3:C:69:THR:HG22	1.78	0.66
2:B:202:ASN:HD22	2:B:205:ALA:H	1.43	0.66
22:V:24:G:C6	22:V:25:C:C4	2.84	0.66
22:V:25:C:N3	22:V:26:A:C8	2.64	0.66
1:A:944:G:N1	1:A:1338:G:OP2	2.29	0.65
1:A:580:C:H5''	15:O:57:ARG:HH11	1.61	0.65
4:D:12:ARG:HG2	4:D:33:ILE:HA	1.78	0.65
1:A:1054:C:C2	22:V:34:A:O4'	2.49	0.65
1:A:292:G:O2'	1:A:609:A:N6	2.29	0.65
15:O:25:GLU:OE2	15:O:76:ARG:NH1	2.29	0.65
22:V:73:A:O2'	22:V:74:C:OP2	2.13	0.65
1:A:230:G:C3'	16:P:31:ARG:HH22	2.08	0.65
22:V:42:C:H2'	22:V:42:C:O2	1.94	0.65
1:A:652:U:HO2'	1:A:752:G:H1	1.44	0.65
2:B:71:THR:HG21	2:B:93:HIS:H	1.60	0.65
1:A:401:C:N4	1:A:402:G:O6	2.30	0.65
8:H:74:ILE:HG13	8:H:128:VAL:HG12	1.79	0.65
1:A:975:A:H1'	1:A:1358:U:H1'	1.79	0.64
4:D:125:ASN:ND2	4:D:140:ASP:OD1	2.30	0.64
1:A:375:U:H4'	16:P:6:LEU:CB	2.27	0.64
22:V:27:G:C2	22:V:28:G:N7	2.65	0.64
1:A:392:C:O2'	1:A:483:C:O2'	2.11	0.64
3:C:21:TRP:NE1	3:C:35:ASP:OD2	2.30	0.64
13:M:78:ARG:NH1	13:M:82:LEU:HD11	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:G:N2	1:A:97:G:N7	2.45	0.64
28:3:29:SER:OG	28:3:40:ARG:HD3	1.97	0.64
23:W:72:G:H3'	23:W:73:A:C5'	2.26	0.64
1:A:185:U:O4	1:A:186:C:N4	2.30	0.64
1:A:450:G:H21	16:P:13:LYS:HZ3	0.65	0.64
1:A:553:A:O2'	12:L:25:ALA:O	2.10	0.64
1:A:1319:A:H5'	19:S:69:LYS:HZ3	1.63	0.64
1:A:15:G:N2	5:E:21:SER:O	2.30	0.64
1:A:521:G:OP2	12:L:50:LYS:NZ	2.30	0.64
11:K:122:PRO:HD2	21:U:34:ARG:HG2	1.80	0.64
11:K:125:LYS:HB3	21:U:33:ARG:HH11	1.63	0.64
28:3:25:VAL:HG13	28:3:26:THR:N	2.12	0.64
1:A:208:U:H3	1:A:211:G:H22	1.45	0.64
2:B:23:ASN:ND2	2:B:191:ASP:OD2	2.30	0.64
17:Q:60:ILE:HG22	17:Q:74:LEU:HA	1.80	0.64
18:R:35:SER:HA	18:R:71:ASP:HB2	1.80	0.64
1:A:606:G:N2	1:A:632:U:OP1	2.30	0.63
3:C:123:LEU:HD13	3:C:195:ILE:HG21	1.79	0.63
22:V:74:C:O2'	22:V:75:C:OP1	2.12	0.63
1:A:491:G:OP1	4:D:147:LYS:NZ	2.32	0.63
17:Q:46:HIS:HB3	17:Q:73:THR:HG22	1.79	0.63
11:K:34:THR:HG22	11:K:40:ALA:HA	1.79	0.63
25:0:68:LEU:HD23	25:0:71:LEU:CD1	2.22	0.63
1:A:6:G:H4'	1:A:298:A:H4'	1.80	0.63
1:A:1238:A:OP1	1:A:1335:U:O2'	2.15	0.63
1:A:738:C:OP1	6:F:68:GLN:NE2	2.32	0.63
24:X:19:U:C2	24:X:20:C:N4	2.66	0.63
1:A:1228:C:H5''	13:M:106:ARG:HH22	1.63	0.63
10:J:8:ILE:HG22	10:J:100:ILE:HA	1.81	0.63
16:P:59:HIS:HE1	16:P:63:GLN:HE22	1.45	0.63
1:A:1201:A:H1'	1:A:1202:U:OP2	1.99	0.62
1:A:974:A:H8	1:A:974:A:OP1	1.82	0.62
1:A:1243:C:H2'	1:A:1244:G:H8	1.63	0.62
1:A:182:A:OP2	1:A:182:A:H2'	2.00	0.62
19:S:5:LYS:HE2	19:S:6:LYS:HE2	1.81	0.62
2:B:79:VAL:HA	2:B:213:LEU:HD21	1.80	0.62
1:A:375:U:H1'	16:P:17:TYR:CE2	2.32	0.62
1:A:392:C:P	16:P:12:LYS:CG	2.85	0.62
1:A:941:G:H1	9:I:125:GLN:CD	2.03	0.62
3:C:84:GLU:OE1	3:C:87:ARG:NH2	2.31	0.62
6:F:6:ILE:HG12	6:F:89:VAL:HG23	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:81:GLY:O	17:Q:35:LYS:NZ	2.23	0.62
11:K:124:LYS:HB3	21:U:34:ARG:HH21	1.64	0.62
16:P:79:ASN:O	16:P:80:LYS:HB2	1.98	0.62
1:A:405:U:OP1	1:A:406:G:O2'	2.16	0.62
4:D:90:LEU:HD11	4:D:196:GLU:OE2	1.98	0.62
8:H:101:ALA:HB3	8:H:112:ASP:HB3	1.81	0.62
9:I:111:GLU:O	9:I:112:ARG:HB3	1.99	0.62
27:2:5:ILE:CG2	27:2:57:VAL:HG13	2.30	0.62
18:R:23:LYS:NZ	18:R:64:LEU:HD12	2.15	0.62
22:V:75:C:H2'	22:V:76:A:C8	2.34	0.62
3:C:10:ARG:NH2	3:C:174:LEU:O	2.33	0.62
4:D:173:ASP:HB3	4:D:178:GLU:H	1.63	0.62
16:P:22:ALA:HB2	16:P:32:PHE:HA	1.80	0.62
24:X:12:C:P	24:X:12:C:H3'	2.40	0.62
28:3:25:VAL:HG13	28:3:26:THR:H	1.64	0.62
32:8:3:VAL:CG2	32:8:36:ARG:NH1	2.59	0.62
1:A:123:U:OP1	1:A:311:C:O2'	2.16	0.62
13:M:48:SER:HB2	13:M:51:GLN:HB2	1.81	0.62
1:A:592:G:O6	1:A:647:C:N4	2.33	0.61
9:I:113:LYS:HB3	9:I:117:LEU:HD21	1.81	0.61
9:I:122:ARG:HH21	9:I:124:PRO:HA	1.64	0.61
16:P:57:ILE:O	16:P:61:VAL:HG23	2.00	0.61
21:U:27:VAL:O	21:U:31:VAL:HG13	1.92	0.61
1:A:468:A:H5'	1:A:469:C:OP2	1.99	0.61
1:A:375:U:C4'	16:P:6:LEU:HD23	2.29	0.61
1:A:1148:U:H1'	9:I:17:ARG:NH1	2.15	0.61
1:A:1348:U:H2'	1:A:1349:A:H8	1.64	0.61
4:D:152:SER:HA	4:D:155:LYS:HZ3	1.65	0.61
10:J:10:LEU:HB2	10:J:72:ARG:HB2	1.82	0.61
1:A:539:A:H8	1:A:539:A:OP2	1.83	0.61
22:V:56:C:N3	22:V:57:G:C6	2.69	0.61
24:X:19:U:H5'	24:X:19:U:C6	2.30	0.61
1:A:1156:G:O2'	1:A:1180:A:N1	2.31	0.61
1:A:520:A:OP2	12:L:47:ALA:HB1	2.00	0.61
22:V:74:C:H4'	22:V:75:C:OP1	1.99	0.61
24:X:21:A:H3'	24:X:22:A:C8	2.35	0.61
12:L:5:GLN:O	12:L:9:LYS:N	2.34	0.61
22:V:68:C:C2	22:V:69:G:C8	2.88	0.61
1:A:1003:G:N2	1:A:1004:A:O2'	2.34	0.61
1:A:1454:G:H2'	1:A:1455:G:H8	1.64	0.61
1:A:698:G:H5'	1:A:699:C:OP2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:U:O2'	10:J:58:ASN:ND2	2.34	0.61
2:B:70:GLY:HA3	2:B:163:ILE:HG22	1.82	0.61
17:Q:53:GLY:N	17:Q:56:ASP:OD2	2.34	0.61
1:A:1320:C:H5''	19:S:69:LYS:HD2	1.83	0.61
1:A:600:A:OP1	8:H:88:LYS:N	2.33	0.60
2:B:187:ASP:OD2	2:B:203:ASP:HB3	2.01	0.60
4:D:182:LYS:NZ	4:D:183:ARG:HH11	1.99	0.60
16:P:37:GLY:HA2	16:P:51:ARG:NH1	2.16	0.60
1:A:652:U:O4	1:A:752:G:O2'	2.15	0.60
1:A:701:U:O2	1:A:703:G:N1	2.33	0.60
6:F:71:ILE:HA	6:F:74:LEU:HD12	1.82	0.60
16:P:67:ILE:CG2	16:P:72:ALA:HB2	2.31	0.60
4:D:121:ALA:O	4:D:145:ARG:N	2.29	0.60
1:A:1231:G:H5''	9:I:128:LYS:HD3	1.83	0.60
9:I:25:GLY:HA3	9:I:57:VAL:HG13	1.83	0.60
17:Q:63:CYS:O	17:Q:71:SER:OG	2.17	0.60
11:K:125:LYS:HG2	21:U:33:ARG:HD2	1.82	0.60
17:Q:25:GLU:OE2	17:Q:38:LYS:HG2	2.01	0.60
18:R:22:TYR:CZ	18:R:23:LYS:HD3	2.37	0.60
1:A:1100:C:N4	1:A:1103:C:OP1	2.34	0.60
2:B:65:LYS:HD2	2:B:89:PHE:HE2	1.65	0.60
3:C:40:GLN:OE1	3:C:44:LYS:NZ	2.34	0.60
8:H:17:GLN:HE22	8:H:62:LEU:HD22	1.66	0.60
10:J:14:ASP:OD1	10:J:15:HIS:N	2.34	0.60
10:J:84:VAL:HA	10:J:87:LEU:HB2	1.83	0.60
1:A:148:G:O2'	1:A:149:A:OP1	2.19	0.60
3:C:80:GLY:O	3:C:83:VAL:HG22	2.01	0.60
5:E:158:LYS:HB3	8:H:63:LYS:NZ	2.16	0.60
12:L:99:GLY:HA3	12:L:117:GLY:HA3	1.84	0.60
18:R:23:LYS:HZ3	18:R:64:LEU:HD12	1.67	0.60
1:A:14:U:O2	1:A:14:U:H2'	3.14	0.60
19:S:62:THR:HG22	19:S:64:GLU:H	1.65	0.60
1:A:662:U:O2'	1:A:836:G:OP1	2.18	0.60
1:A:960:U:H4'	1:A:961:U:OP2	2.00	0.60
21:U:16:ARG:HA	21:U:19:LYS:NZ	2.17	0.60
22:V:27:G:N2	22:V:28:G:C6	2.70	0.60
1:A:1265:C:H2'	1:A:1266:G:H8	1.67	0.59
1:A:947:G:O2'	1:A:1306:A:O2'	2.20	0.59
3:C:59:PRO:HB2	3:C:61:LYS:NZ	2.17	0.59
5:E:88:HIS:CD2	5:E:137:ARG:HG3	2.36	0.59
18:R:25:ILE:HG12	18:R:29:LYS:HE3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1397:C:OP2	5:E:28:ARG:NH2	2.35	0.59
1:A:434:U:H5'	1:A:435:A:OP2	2.02	0.59
1:A:437:U:OP1	4:D:151:GLN:NE2	2.35	0.59
1:A:450:G:H22	16:P:13:LYS:NZ	1.94	0.59
16:P:20:VAL:CG2	16:P:32:PHE:HB2	2.32	0.59
1:A:1332:A:O2'	1:A:1333:A:OP1	2.19	0.59
3:C:18:ASN:ND2	14:N:89:ARG:O	2.35	0.59
1:A:543:U:OP1	4:D:13:ARG:NE	2.36	0.59
1:A:430:A:P	4:D:7:LYS:H	2.25	0.59
13:M:36:ALA:HB3	13:M:38:ILE:HG12	1.83	0.59
15:O:48:ASP:OD2	15:O:51:SER:HB2	2.02	0.59
1:A:230:G:C3'	16:P:31:ARG:NH2	2.64	0.59
1:A:137:U:C1'	16:P:64:GLY:HA3	2.33	0.59
9:I:106:ASP:OD2	9:I:108:ARG:HB2	2.03	0.59
1:A:1341:U:O2'	9:I:128:LYS:N	2.36	0.59
24:X:19:U:C5'	24:X:19:U:C6	2.86	0.59
1:A:1405:G:H1	1:A:1496:C:H42	1.49	0.59
1:A:528:C:H41	12:L:45:ASN:ND2	2.00	0.59
1:A:1397:C:N4	24:X:21:A:OP2	2.35	0.59
1:A:1329:A:H5''	13:M:25:GLY:H	1.67	0.59
4:D:13:ARG:HA	4:D:37:PRO:HG3	1.83	0.59
9:I:34:LEU:O	9:I:38:PHE:N	2.36	0.59
1:A:1111:A:HO2'	1:A:1112:C:H6	1.49	0.58
1:A:100:G:N2	1:A:101:A:H1'	7.06	0.58
1:A:430:A:OP2	4:D:7:LYS:N	2.23	0.58
1:A:469:C:H2'	1:A:470:C:O4'	2.04	0.58
24:X:13:U:H4'	24:X:13:U:OP2	2.03	0.58
1:A:992:U:O2'	1:A:1043:G:O6	2.18	0.58
1:A:776:G:N2	1:A:802:A:OP2	2.36	0.58
1:A:974:A:OP2	14:N:80:ARG:NH1	2.37	0.58
22:V:27:G:C2	22:V:28:G:C5	2.91	0.58
23:W:72:G:C3'	23:W:73:A:H5'	2.34	0.58
1:A:1161:C:H42	1:A:1175:G:H1	1.51	0.58
1:A:753:A:OP1	15:O:68:TYR:OH	2.17	0.58
1:A:998:C:N3	1:A:1043:G:N2	2.43	0.58
16:P:59:HIS:CE1	16:P:63:GLN:NE2	2.71	0.58
1:A:1164:G:H1	1:A:1172:C:H42	1.51	0.58
1:A:1263:C:H42	1:A:1272:G:H1	1.51	0.58
1:A:521:G:P	12:L:50:LYS:HZ1	2.26	0.58
7:G:110:ARG:O	7:G:118:ARG:NE	2.36	0.58
16:P:5:ARG:HA	16:P:68:SER:OG	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:27:VAL:O	21:U:27:VAL:HG12	2.03	0.58
1:A:1125:U:H2'	1:A:1126:U:H2'	1.86	0.58
5:E:12:GLU:OE2	5:E:63:MET:HG2	2.03	0.58
22:V:25:C:C4	22:V:26:A:N7	2.70	0.58
5:E:47:PHE:HZ	5:E:137:ARG:NH1	2.01	0.58
9:I:112:ARG:CZ	9:I:114:LYS:CG	2.80	0.58
17:Q:20:ILE:HD12	17:Q:47:ASP:OD2	2.03	0.58
22:V:41:C:N3	22:V:42:C:C5	2.71	0.58
2:B:29:PHE:HB3	2:B:44:LYS:HD2	1.85	0.58
1:A:1100:C:OP2	2:B:94:ARG:NE	2.37	0.58
9:I:57:VAL:H	9:I:60:LEU:HD11	1.68	0.58
3:C:185:THR:HG22	3:C:198:LYS:HG2	1.86	0.58
6:F:21:MET:HB3	6:F:25:TYR:HE2	1.68	0.58
11:K:35:ASP:OD1	11:K:36:ARG:N	2.34	0.58
20:T:70:LYS:HG3	20:T:73:ARG:HH21	1.69	0.58
1:A:1002:G:H2'	1:A:1003:G:H8	1.68	0.58
1:A:1309:G:H2'	1:A:1310:G:H8	1.69	0.58
1:A:1454:G:H2'	1:A:1455:G:C8	2.39	0.58
1:A:254:G:H4'	1:A:255:G:OP1	2.04	0.58
1:A:570:G:O3'	1:A:819:A:O2'	2.21	0.58
4:D:100:VAL:HG21	4:D:136:VAL:HG11	1.85	0.58
7:G:137:ARG:NH2	7:G:138:GLU:OE2	2.37	0.58
16:P:19:VAL:HG13	16:P:37:GLY:C	2.24	0.58
22:V:24:G:C5	22:V:25:C:C5	2.91	0.58
1:A:474:G:C5	1:A:475:C:H1'	2.39	0.57
1:A:941:G:N1	9:I:125:GLN:OE1	2.36	0.57
1:A:142:G:O2'	1:A:195:A:N6	2.37	0.57
3:C:178:ARG:HE	3:C:206:ILE:HB	1.70	0.57
4:D:182:LYS:NZ	4:D:183:ARG:HH12	2.00	0.57
16:P:77:GLU:C	16:P:79:ASN:H	2.07	0.57
28:3:25:VAL:O	28:3:26:THR:OG1	2.18	0.57
1:A:6:G:N1	5:E:99:SER:OG	2.37	0.57
1:A:876:C:OP1	8:H:14:ARG:NH1	2.37	0.57
13:M:89:ARG:HH11	13:M:94:LEU:HB2	1.68	0.57
22:V:29:G:C2	22:V:30:G:C8	2.92	0.57
1:A:136:C:H4'	16:P:1:MET:HG3	1.86	0.57
23:W:28:C:N3	23:W:43:G:N2	2.52	0.57
16:P:10:GLY:O	16:P:11:ALA:HB2	2.05	0.57
1:A:123:U:H3	1:A:238:A:H61	1.53	0.57
1:A:900:A:H2'	1:A:901:A:C8	2.40	0.57
5:E:14:LEU:HA	5:E:36:THR:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:28:THR:HG22	10:J:31:ARG:NH1	2.20	0.57
1:A:470:C:H2'	1:A:471:U:H6	1.68	0.57
10:J:63:ASP:OD2	10:J:65:TYR:CZ	2.58	0.57
1:A:640:A:N6	1:A:641:U:O4	2.38	0.57
1:A:667:G:H2'	1:A:668:G:H8	1.70	0.57
1:A:707:U:H5''	11:K:21:HIS:ND1	2.19	0.57
22:V:33:U:C2'	22:V:34:A:C2	2.80	0.57
1:A:885:G:H1	1:A:912:C:H42	1.53	0.57
5:E:110:MET:HA	5:E:113:VAL:HG22	1.87	0.57
7:G:14:ASP:HB2	7:G:23:ALA:HB2	1.87	0.57
1:A:1362:A:H2'	1:A:1362:A:OP2	2.05	0.57
1:A:967:C:OP2	1:A:968:A:O2'	2.14	0.57
21:U:27:VAL:HG13	21:U:31:VAL:CB	2.35	0.57
1:A:1111:A:N1	3:C:176:THR:HG22	2.20	0.56
1:A:1309:G:H2'	1:A:1310:G:C8	2.41	0.56
6:F:5:GLU:HB2	6:F:90:MET:HB2	1.86	0.56
10:J:6:ILE:HB	10:J:76:ILE:HD11	1.87	0.56
19:S:35:ARG:HH12	19:S:74:ALA:HB3	1.69	0.56
1:A:1078:U:H1'	5:E:134:ASN:HD21	1.71	0.56
1:A:1347:G:O6	9:I:11:ARG:NH2	2.37	0.56
1:A:224:U:H2'	1:A:225:C:C6	2.39	0.56
7:G:134:VAL:O	7:G:138:GLU:HG2	2.04	0.56
1:A:231:U:P	16:P:31:ARG:NH2	2.78	0.56
11:K:116:PRO:CD	21:U:27:VAL:HG21	2.32	0.56
22:V:28:G:C6	22:V:29:G:N7	2.73	0.56
5:E:35:LEU:HD11	5:E:133:ILE:HD13	1.87	0.56
22:V:54:U:H2'	22:V:55:U:C2	2.39	0.56
2:B:66:ILE:HB	2:B:88:GLN:HG2	1.86	0.56
15:O:79:ARG:HA	15:O:82:GLU:OE2	2.05	0.56
1:A:1200:C:H5''	1:A:1201:A:H3'	1.86	0.56
6:F:4:TYR:HA	6:F:91:ARG:HA	1.88	0.56
1:A:1271:A:H2'	1:A:1272:G:H8	1.70	0.56
1:A:1342:C:C5'	9:I:126:PHE:HA	2.35	0.56
1:A:483:C:OP2	1:A:484:G:O2'	2.18	0.56
1:A:952:U:H2'	1:A:953:G:H8	1.71	0.56
12:L:42:LYS:HG2	12:L:43:LYS:HG3	1.86	0.56
10:J:28:THR:HA	10:J:31:ARG:HH11	1.69	0.56
14:N:66:THR:HG23	14:N:68:ARG:H	1.70	0.56
1:A:1348:U:H2'	1:A:1349:A:C8	2.40	0.56
1:A:400:C:O2'	1:A:622:A:O2'	2.24	0.56
1:A:59:A:H3'	1:A:331:G:H22	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:18:LEU:HD22	4:D:63:ILE:HD13	1.86	0.56
19:S:5:LYS:HG2	19:S:6:LYS:HG2	1.86	0.56
1:A:439:U:H5'	4:D:119:HIS:HD2	1.70	0.56
19:S:32:THR:HG22	19:S:34:SER:H	1.70	0.56
22:V:28:G:N1	22:V:29:G:C5	2.74	0.56
22:V:38:A:O2'	22:V:39:U:H5'	2.06	0.56
1:A:109:A:H4'	1:A:110:C:OP2	2.04	0.56
1:A:1348:U:O5'	9:I:111:GLU:CG	2.47	0.56
14:N:55:SER:HB3	14:N:58:ARG:HG2	1.86	0.56
11:K:125:LYS:HB3	21:U:33:ARG:NH1	2.20	0.56
1:A:1148:U:H1'	9:I:17:ARG:HH11	1.71	0.56
16:P:67:ILE:HG21	16:P:72:ALA:HB2	1.88	0.56
22:V:41:C:C2	22:V:42:C:C6	2.94	0.56
1:A:149:A:H2'	1:A:150:U:H6	1.70	0.55
1:A:181:A:O2'	1:A:194:C:N4	2.39	0.55
1:A:408:A:H61	1:A:434:U:H3	1.54	0.55
3:C:59:PRO:HB2	3:C:61:LYS:HZ3	1.71	0.55
4:D:94:GLU:HA	4:D:99:ASN:ND2	2.22	0.55
9:I:9:GLY:HA2	9:I:80:HIS:HD2	1.71	0.55
15:O:25:GLU:OE2	15:O:76:ARG:HD2	2.06	0.55
30:6:18:PHE:CE1	30:6:22:MET:HG3	2.41	0.55
1:A:333:U:OP1	20:T:2:ASN:ND2	2.36	0.55
1:A:60:A:H8	1:A:60:A:OP2	1.90	0.55
7:G:110:ARG:HH21	7:G:122:GLU:HA	1.70	0.55
13:M:78:ARG:O	13:M:82:LEU:HG	2.06	0.55
22:V:18:G:O2'	22:V:19:G:C4	2.55	0.55
22:V:37:A:H3'	22:V:38:A:C5'	2.35	0.55
1:A:1243:C:H2'	1:A:1244:G:C8	2.40	0.55
13:M:15:VAL:HG13	13:M:16:ILE:HG12	1.87	0.55
1:A:1149:C:OP2	9:I:10:ARG:NH2	2.33	0.55
1:A:200:G:OP2	1:A:200:G:H8	1.89	0.55
2:B:81:ASP:HA	2:B:84:LEU:HD12	1.89	0.55
6:F:8:PHE:CZ	6:F:60:VAL:HG11	2.41	0.55
1:A:1124:G:O2'	1:A:1145:A:N6	2.39	0.55
1:A:1368:A:H5''	9:I:113:LYS:HB2	1.89	0.55
1:A:1251:A:H1'	1:A:1370:G:H4'	1.88	0.55
1:A:723:U:H3	21:U:48:LYS:HE2	1.72	0.55
8:H:78:SER:OG	8:H:124:ILE:O	2.24	0.55
24:X:18:C:O2	24:X:18:C:H2'	2.07	0.55
4:D:12:ARG:HH12	4:D:37:PRO:HA	1.71	0.55
1:A:950:U:H5''	13:M:100:ARG:HH21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:28:ARG:HE	16:P:29:ASN:ND2	2.01	0.55
22:V:30:G:H1	22:V:40:C:N4	2.02	0.55
1:A:939:G:H1	1:A:1344:C:H42	1.55	0.55
11:K:125:LYS:CB	21:U:33:ARG:HH11	2.20	0.55
1:A:978:A:H61	1:A:1316:G:H21	1.53	0.55
1:A:1318:A:OP2	1:A:1318:A:H8	1.90	0.55
1:A:152:A:N6	1:A:170:U:O2	2.40	0.55
1:A:236:A:H2'	1:A:237:G:C8	2.42	0.55
8:H:12:ARG:HH12	8:H:27:PRO:CD	2.19	0.55
13:M:51:GLN:O	13:M:54:THR:OG1	2.14	0.55
14:N:2:LYS:HE2	14:N:5:MET:HE3	1.89	0.55
16:P:51:ARG:O	16:P:52:LEU:HD12	2.06	0.55
1:A:599:C:H2'	1:A:600:A:C8	2.42	0.55
11:K:45:THR:HG23	11:K:48:GLY:H	1.72	0.55
13:M:58:GLU:HA	13:M:61:LYS:HZ2	1.72	0.55
16:P:10:GLY:HA3	16:P:15:PRO:HA	1.88	0.55
22:V:40:C:H2'	22:V:41:C:C6	2.41	0.55
22:V:24:G:C4	22:V:25:C:C6	2.96	0.54
1:A:1054:C:N3	22:V:34:A:C1'	2.70	0.54
1:A:1263:C:N4	1:A:1272:G:H1	2.05	0.54
1:A:301:G:H2'	1:A:302:G:C8	2.39	0.54
5:E:138:ALA:HA	5:E:141:ASP:HB2	1.88	0.54
5:E:86:GLY:HA3	5:E:141:ASP:HB3	1.89	0.54
8:H:92:PRO:HB2	8:H:94:VAL:HG13	1.89	0.54
10:J:10:LEU:O	10:J:71:LEU:HD12	2.07	0.54
13:M:19:THR:HG21	13:M:26:LYS:HD3	1.89	0.54
15:O:17:ASP:OD1	15:O:18:ALA:N	2.41	0.54
22:V:30:G:N1	22:V:40:C:C4	2.72	0.54
1:A:977:A:N6	1:A:1224:U:O5'	2.40	0.54
1:A:1314:C:OP2	19:S:5:LYS:HE3	2.07	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.42	0.54
9:I:54:VAL:HG12	9:I:93:LEU:HD22	1.89	0.54
19:S:19:GLU:O	19:S:22:VAL:HG22	2.08	0.54
1:A:1069:C:H2'	1:A:1070:U:O4'	2.07	0.54
1:A:453:G:H8	1:A:453:G:OP2	1.91	0.54
1:A:445:G:N2	1:A:489:C:N3	2.48	0.54
1:A:601:G:N2	1:A:638:U:O2	2.40	0.54
2:B:202:ASN:ND2	2:B:208:ALA:HB3	2.22	0.54
5:E:142:GLY:HA2	5:E:145:ASN:HB3	1.89	0.54
1:A:707:U:P	11:K:86:LYS:HZ3	2.31	0.54
1:A:996:A:N1	1:A:1045:C:O2'	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:139:ASP:O	7:G:143:MET:N	2.36	0.54
7:G:68:VAL:HG21	7:G:103:ILE:HD11	1.89	0.54
22:V:41:C:C4	22:V:42:C:C5	2.96	0.54
22:V:72:C:O2	22:V:73:A:N6	2.40	0.54
1:A:1341:U:OP1	23:W:32:A:C5'	2.55	0.54
24:X:13:U:H6	24:X:13:U:H5''	1.73	0.54
3:C:180:ASP:OD2	3:C:203:LYS:HE2	2.07	0.54
3:C:21:TRP:HB3	3:C:58:ARG:HB3	1.90	0.54
4:D:87:GLU:OE1	4:D:187:ARG:NH2	2.40	0.54
7:G:70:PRO:HA	7:G:141:HIS:CE1	2.42	0.54
9:I:78:ILE:O	9:I:82:ILE:HG12	2.08	0.54
13:M:38:ILE:HG21	13:M:51:GLN:HE21	1.71	0.54
1:A:1085:U:H3'	1:A:1086:U:C6	2.43	0.54
1:A:218:U:H4'	1:A:219:U:OP1	2.06	0.54
1:A:429:U:H3	1:A:431:A:H62	1.56	0.54
21:U:27:VAL:CG1	21:U:31:VAL:CG1	2.83	0.54
1:A:408:A:H5''	4:D:7:LYS:NZ	2.23	0.54
1:A:447:G:H21	1:A:487:A:H62	1.56	0.54
1:A:620:C:H5''	1:A:621:A:OP2	2.08	0.54
2:B:187:ASP:OD2	2:B:189:ASN:ND2	2.41	0.54
22:V:19:G:N2	22:V:57:G:H22	2.05	0.54
22:V:36:G:H2'	22:V:37:A:H8	1.71	0.54
9:I:128:LYS:C	23:W:32:A:OP1	2.47	0.54
1:A:1178:G:C5	9:I:98:ARG:NH1	2.76	0.54
11:K:36:ARG:NH1	11:K:82:GLU:OE1	2.41	0.54
1:A:113:G:H21	1:A:353:A:H8	1.55	0.54
1:A:386:C:OP2	1:A:386:C:H6	1.91	0.54
1:A:413:G:OP1	1:A:414:A:H5''	2.08	0.54
4:D:124:VAL:HB	4:D:140:ASP:OD2	2.08	0.54
21:U:26:GLY:O	21:U:27:VAL:HB	2.08	0.54
1:A:100:G:C4	1:A:101:A:C8	3.74	0.53
1:A:680:C:H2'	1:A:681:A:H8	1.73	0.53
22:V:72:C:H4'	22:V:73:A:OP2	2.08	0.53
1:A:1341:U:OP1	23:W:32:A:H5'	2.08	0.53
4:D:84:ASN:ND2	4:D:187:ARG:HH22	2.05	0.53
6:F:12:PRO:HB3	6:F:57:ALA:HA	1.91	0.53
21:U:14:ALA:H	21:U:16:ARG:NH2	2.06	0.53
26:I:45:GLN:O	26:I:47:ARG:N	2.39	0.53
1:A:1113:C:H4'	3:C:13:ILE:HG21	1.90	0.53
4:D:11:SER:O	4:D:15:GLY:N	2.39	0.53
4:D:193:ASP:O	4:D:195:ASN:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1341:U:C2	9:I:126:PHE:HD1	2.26	0.53
12:L:54:VAL:HG11	12:L:81:ILE:HD11	1.90	0.53
1:A:1219:A:OP1	14:N:52:ARG:NH1	2.42	0.53
1:A:468:A:H5''	1:A:469:C:H5	1.74	0.53
12:L:113:ARG:HB2	12:L:118:VAL:HG13	1.91	0.53
16:P:20:VAL:HG21	16:P:32:PHE:HB2	1.90	0.53
24:X:12:C:OP1	24:X:12:C:H2'	2.09	0.53
1:A:1221:G:OP1	1:A:1320:C:N4	2.39	0.53
10:J:26:VAL:HA	10:J:29:ALA:HB3	1.90	0.53
1:A:693:G:P	11:K:126:ARG:HH12	2.26	0.53
21:U:16:ARG:HA	21:U:19:LYS:HZ2	1.72	0.53
1:A:316:C:OP2	1:A:351:G:O2'	2.26	0.53
5:E:152:VAL:HG11	8:H:98:LEU:HG	1.89	0.53
1:A:1458:G:OP1	20:T:29:THR:OG1	2.25	0.53
22:V:28:G:C6	22:V:29:G:C5	2.97	0.53
24:X:15:G:H2'	24:X:16:C:H5'	1.91	0.53
1:A:562:U:O2'	12:L:11:ARG:HB3	2.08	0.53
20:T:32:LYS:HA	20:T:35:TYR:HD2	1.73	0.53
22:V:37:A:H3'	22:V:38:A:H5'	1.91	0.53
14:N:25:GLU:HB3	14:N:30:ILE:HG13	1.91	0.53
1:A:100:G:C6	1:A:101:A:C5	4.23	0.52
1:A:137:U:H1'	16:P:64:GLY:HA3	1.91	0.52
1:A:321:A:N6	1:A:332:G:H1	2.02	0.52
7:G:128:GLU:HB2	7:G:130:LYS:NZ	2.24	0.52
10:J:9:ARG:NH1	10:J:71:LEU:HD21	2.17	0.52
20:T:31:ILE:HG13	20:T:78:LEU:HD11	1.91	0.52
1:A:1469:C:H5''	1:A:1470:U:OP2	2.08	0.52
1:A:151:A:O2'	1:A:152:A:H8	1.91	0.52
1:A:204:G:OP2	1:A:204:G:H3'	2.10	0.52
1:A:510:A:HO2'	1:A:542:G:HO2'	1.57	0.52
1:A:978:A:H61	1:A:1316:G:N2	2.07	0.52
2:B:56:LEU:HD23	2:B:59:ILE:HD11	1.90	0.52
3:C:166:TRP:HH2	3:C:168:ARG:NH1	2.07	0.52
3:C:49:ALA:O	3:C:71:ARG:NH2	2.42	0.52
16:P:2:VAL:HG23	16:P:65:ALA:HA	1.92	0.52
1:A:462:G:H1	1:A:470:C:H42	1.55	0.52
19:S:23:GLU:HG2	19:S:24:SER:N	2.25	0.52
22:V:28:G:C4	22:V:29:G:C8	2.98	0.52
1:A:197:A:H4'	1:A:198:G:OP1	2.10	0.52
1:A:382:A:H2'	1:A:383:A:H8	1.74	0.52
6:F:50:PRO:HB3	6:F:53:LYS:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:66:GLY:O	13:M:70:ARG:HG3	2.10	0.52
1:A:1002:G:N2	1:A:1038:C:N3	2.57	0.52
2:B:70:GLY:HA2	2:B:168:GLU:HG3	1.91	0.52
2:B:56:LEU:HD22	2:B:66:ILE:HD13	1.90	0.52
7:G:110:ARG:HB3	7:G:118:ARG:HG2	1.91	0.52
1:A:202:G:C2	1:A:203:G:H1'	2.45	0.52
1:A:39:G:N2	1:A:404:G:H1'	2.24	0.52
4:D:169:TRP:NE1	4:D:185:PRO:HG3	2.25	0.52
11:K:82:GLU:HG3	11:K:108:ASN:HB2	1.91	0.52
1:A:107:G:O6	20:T:9:ARG:HD2	2.10	0.52
1:A:1305:G:O2'	1:A:1306:A:O4'	2.27	0.52
1:A:1510:C:H2'	1:A:1511:G:C8	2.45	0.52
1:A:374:A:H3'	1:A:375:U:C6	2.45	0.52
2:B:115:ASP:O	2:B:118:THR:OG1	2.14	0.52
7:G:110:ARG:HD3	7:G:112:ASP:OD2	2.09	0.52
22:V:42:C:O2	22:V:42:C:C2'	2.58	0.52
22:V:49:C:N3	22:V:50:U:C5	2.78	0.52
1:A:470:C:H2'	1:A:471:U:C6	2.44	0.52
10:J:37:ARG:HB2	10:J:75:ASP:HB2	1.92	0.52
1:A:227:G:O2'	16:P:63:GLN:CG	2.58	0.52
22:V:38:A:O2'	22:V:39:U:C5'	2.58	0.52
22:V:53:G:C2	22:V:62:C:C2	2.97	0.52
2:B:56:LEU:HD12	2:B:219:THR:HG21	1.90	0.52
3:C:141:MET:HG3	3:C:169:GLU:OE2	2.10	0.52
1:A:1347:G:O3'	9:I:111:GLU:HG2	2.10	0.52
1:A:1492:A:H8	24:X:18:C:HO2'	1.57	0.52
1:A:1252:A:H61	1:A:1285:A:H61	1.58	0.52
1:A:109:A:C6	1:A:326:G:C6	2.98	0.52
3:C:106:ARG:NH2	3:C:111:ASP:OD2	2.43	0.52
9:I:51:LEU:HD13	9:I:56:MET:HG3	1.92	0.52
16:P:12:LYS:O	16:P:13:LYS:HB2	2.10	0.52
17:Q:14:ASP:OD2	17:Q:54:ILE:HG13	2.10	0.52
25:O:68:LEU:CD2	25:O:71:LEU:HD12	2.25	0.51
1:A:1054:C:C4	22:V:34:A:N9	2.78	0.51
1:A:1256:A:C6	1:A:1278:G:H2'	2.44	0.51
1:A:396:C:O2'	1:A:398:U:OP1	2.26	0.51
3:C:87:ARG:HG3	3:C:98:ALA:HB3	1.91	0.51
11:K:48:GLY:O	11:K:68:ARG:NH1	2.43	0.51
1:A:262:A:H4'	20:T:69:ASN:HB2	1.92	0.51
1:A:1085:U:H3'	1:A:1086:U:H6	1.76	0.51
1:A:1251:A:O2'	1:A:1370:G:O5'	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:U:H4'	16:P:6:LEU:HB2	1.91	0.51
4:D:68:GLU:OE2	4:D:203:TYR:OH	2.19	0.51
7:G:71:THR:HG23	7:G:72:VAL:HG13	1.93	0.51
13:M:89:ARG:HH11	13:M:94:LEU:CB	2.23	0.51
14:N:87:ALA:HB2	14:N:92:ILE:HD12	1.91	0.51
1:A:264:C:O2'	17:Q:65:PRO:O	2.25	0.51
22:V:2:C:H2'	22:V:2:C:O2	2.09	0.51
22:V:74:C:H3'	22:V:75:C:C5	2.45	0.51
1:A:1404:C:O2	1:A:1519:A:O2'	2.28	0.51
1:A:83:C:H5'	1:A:84:U:H5	1.75	0.51
1:A:878:A:OP1	8:H:79:ARG:NH1	2.43	0.51
1:A:96:U:H2'	1:A:97:G:C8	2.45	0.51
1:A:675:A:H1'	11:K:117:HIS:CE1	2.45	0.51
12:L:53:ARG:HB3	12:L:61:GLU:OE2	2.10	0.51
21:U:29:ALA:C	21:U:31:VAL:N	2.57	0.51
22:V:5:G:C2	22:V:6:G:C8	2.99	0.51
1:A:1367:C:O5'	9:I:117:LEU:HD12	2.11	0.51
1:A:932:C:O2	1:A:1386:G:N2	2.43	0.51
1:A:392:C:P	16:P:12:LYS:HG3	2.49	0.51
1:A:946:A:H2'	1:A:947:G:C8	2.44	0.51
3:C:33:ASP:OD2	14:N:64:ARG:HD2	2.10	0.51
4:D:152:SER:HA	4:D:155:LYS:HZ1	1.74	0.51
16:P:6:LEU:HG	16:P:17:TYR:CB	2.40	0.51
19:S:35:ARG:NH1	19:S:74:ALA:HB3	2.25	0.51
1:A:1054:C:OP2	1:A:1197:A:OP2	2.28	0.51
1:A:201:G:N2	1:A:469:C:O2	2.43	0.51
3:C:20:THR:HB	3:C:57:GLU:HA	1.92	0.51
22:V:27:G:H2'	22:V:28:G:H8	1.75	0.51
22:V:73:A:N3	22:V:73:A:C2'	2.74	0.51
1:A:1240:U:H5''	1:A:1241:G:OP2	2.11	0.51
1:A:149:A:H2'	1:A:150:U:C6	2.46	0.51
1:A:1510:C:H2'	1:A:1511:G:H8	1.75	0.51
1:A:329:A:H2'	1:A:329:A:N3	2.26	0.51
9:I:21:LYS:O	9:I:60:LEU:HA	2.11	0.51
22:V:19:G:H21	22:V:57:G:N2	2.05	0.51
24:X:18:C:H6	24:X:18:C:H5''	1.73	0.51
1:A:541:G:H5'	1:A:542:G:OP2	2.10	0.51
8:H:13:ILE:O	8:H:17:GLN:HG2	2.10	0.51
1:A:130:A:OP1	17:Q:64:ARG:HD2	2.11	0.51
1:A:1319:A:H5'	19:S:69:LYS:NZ	2.26	0.51
1:A:219:U:H2'	1:A:220:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:G:H8	1:A:540:G:OP2	1.93	0.51
10:J:21:ALA:O	10:J:25:ILE:HG12	2.10	0.51
14:N:51:PRO:O	14:N:53:ASP:N	2.43	0.51
1:A:1054:C:N3	22:V:34:A:N9	2.58	0.51
1:A:1098:C:OP2	2:B:142:LYS:HE3	2.10	0.51
1:A:1254:A:H2'	1:A:1255:G:C8	2.46	0.51
1:A:618:C:H5''	1:A:619:U:H5''	1.92	0.51
4:D:2:ARG:CZ	4:D:114:ARG:HD2	2.40	0.51
14:N:52:ARG:HG2	14:N:58:ARG:HH12	1.76	0.51
1:A:228:A:O2'	16:P:60:TRP:HZ3	1.94	0.51
1:A:1338:G:N7	23:W:41:C:O2'	2.39	0.51
1:A:1096:C:O2	1:A:1170:A:O2'	2.28	0.51
1:A:1492:A:H4'	1:A:1493:A:OP1	2.11	0.51
8:H:104:SER:HB2	8:H:125:ILE:HD11	1.92	0.51
13:M:79:LEU:HD23	13:M:82:LEU:HD12	1.92	0.51
14:N:22:LYS:HE2	14:N:23:ARG:HH12	1.73	0.51
1:A:1134:G:N2	1:A:1140:C:N3	2.58	0.50
16:P:20:VAL:HG23	16:P:34:GLU:O	2.10	0.50
22:V:74:C:H2'	22:V:74:C:O2	2.09	0.50
1:A:1342:C:H5'	1:A:1343:G:OP2	2.11	0.50
1:A:508:U:H5''	4:D:50:TYR:HD2	1.75	0.50
3:C:64:ARG:HG2	3:C:99:GLN:HB3	1.93	0.50
1:A:1026:G:H2'	1:A:1027:C:O4'	2.12	0.50
1:A:201:G:H21	1:A:469:C:H1'	1.76	0.50
1:A:81:A:H61	1:A:87:C:HO2'	1.57	0.50
2:B:100:LEU:HB2	2:B:174:GLU:OE2	2.11	0.50
5:E:24:VAL:HG12	5:E:26:GLY:H	1.76	0.50
1:A:455:G:H8	1:A:455:G:OP2	1.94	0.50
2:B:101:THR:HG23	2:B:174:GLU:OE2	2.12	0.50
2:B:55:GLU:HA	2:B:58:LYS:HE3	1.94	0.50
14:N:20:PHE:HA	14:N:24:ALA:HA	1.94	0.50
20:T:34:VAL:O	20:T:38:ILE:HG12	2.11	0.50
1:A:1343:G:O4'	9:I:125:GLN:HA	2.11	0.50
1:A:391:G:C5	1:A:392:C:C4	2.99	0.50
1:A:478:A:O2'	1:A:479:U:OP1	2.28	0.50
5:E:37:VAL:HG21	5:E:113:VAL:HG12	1.93	0.50
1:A:375:U:H4'	16:P:6:LEU:HD23	1.93	0.50
22:V:24:G:C2	22:V:25:C:C2	3.00	0.50
27:2:3:LYS:O	27:2:4:THR:OG1	2.26	0.50
1:A:367:U:OP1	1:A:395:C:O2'	2.28	0.50
1:A:676:A:H5''	11:K:114:PRO:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:A:N3	1:A:1512:U:O2'	2.43	0.50
11:K:20:ALA:HB2	11:K:81:LEU:HD22	1.94	0.50
15:O:17:ASP:HB3	15:O:20:ASP:OD1	2.12	0.50
11:K:125:LYS:CG	21:U:33:ARG:HH11	2.25	0.50
22:V:30:G:C2	22:V:41:C:C2	3.00	0.50
7:G:137:ARG:NH1	7:G:141:HIS:CE1	2.76	0.50
11:K:23:HIS:CD2	11:K:24:ALA:H	2.29	0.50
14:N:25:GLU:HA	14:N:28:ALA:HB3	1.93	0.50
16:P:22:ALA:CB	16:P:32:PHE:HA	2.41	0.50
18:R:24:ASP:OD2	18:R:27:THR:HG23	2.11	0.50
1:A:108:G:H5'	1:A:109:A:H2	1.76	0.50
1:A:116:A:OP2	1:A:289:G:OP2	2.30	0.50
1:A:1210:C:H2'	1:A:1211:U:C6	2.47	0.50
4:D:169:TRP:CE2	4:D:185:PRO:HG3	2.47	0.50
1:A:1348:U:P	9:I:111:GLU:OE2	2.69	0.50
16:P:78:VAL:HG22	16:P:78:VAL:O	2.12	0.50
17:Q:7:LEU:HD21	17:Q:24:ILE:HD13	1.94	0.50
22:V:53:G:N3	22:V:53:G:H2'	2.26	0.50
9:I:4:GLN:HE22	9:I:21:LYS:HE3	1.77	0.50
11:K:113:THR:HG21	21:U:28:LEU:HD11	1.93	0.50
16:P:12:LYS:HG2	16:P:13:LYS:HG2	1.94	0.50
22:V:40:C:O2	22:V:40:C:H2'	2.12	0.50
1:A:701:U:O2'	1:A:702:A:OP2	2.21	0.49
1:A:718:A:C8	11:K:117:HIS:CD2	3.00	0.49
4:D:23:GLY:HA2	4:D:160:LEU:HD23	1.93	0.49
6:F:18:VAL:HG21	6:F:58:HIS:CD2	2.47	0.49
1:A:1349:A:OP2	9:I:119:LYS:HD2	2.11	0.49
16:P:20:VAL:HG21	16:P:32:PHE:CG	2.47	0.49
22:V:25:C:N4	22:V:26:A:N7	2.60	0.49
1:A:1371:G:H5''	9:I:69:GLY:HA2	1.93	0.49
1:A:843:U:P	1:A:846:G:H1	2.34	0.49
3:C:110:LEU:HD21	3:C:145:ALA:HB2	1.93	0.49
1:A:374:A:H1'	1:A:451:A:OP2	2.13	0.49
1:A:588:G:O2'	1:A:589:U:O5'	2.28	0.49
4:D:98:ASP:OD1	4:D:99:ASN:N	2.45	0.49
7:G:73:GLU:OE1	7:G:94:ARG:NE	2.33	0.49
13:M:111:PRO:HD2	13:M:113:LYS:NZ	2.27	0.49
16:P:20:VAL:HG21	16:P:32:PHE:CB	2.41	0.49
22:V:64:A:C2	22:V:65:G:C8	3.00	0.49
23:W:37:G:H22	24:X:13:U:H3	1.60	0.49
1:A:1030:U:H5'	1:A:1031:C:C5	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:598:U:H2'	1:A:599:C:C6	2.47	0.49
2:B:71:THR:HG23	2:B:76:SER:HA	1.94	0.49
3:C:34:SER:OG	3:C:58:ARG:NH1	2.34	0.49
7:G:99:ALA:O	7:G:103:ILE:HG12	2.11	0.49
19:S:24:SER:HB3	19:S:27:LYS:NZ	2.28	0.49
22:V:68:C:N3	22:V:69:G:N7	2.60	0.49
1:A:1154:G:H2'	1:A:1155:A:H8	1.77	0.49
1:A:189:A:H2'	1:A:190:A:O4'	2.13	0.49
1:A:297:G:N2	1:A:300:A:OP2	2.45	0.49
1:A:667:G:H4'	15:O:50:HIS:HD2	1.78	0.49
1:A:560:A:H61	5:E:94:PHE:HE2	1.61	0.49
3:C:22:PHE:CZ	10:J:11:LYS:HG2	2.48	0.49
16:P:61:VAL:HA	16:P:65:ALA:H	1.76	0.49
1:A:1129:C:N4	1:A:1143:G:H1	2.07	0.49
1:A:1234:C:H1'	1:A:1364:U:H6	1.76	0.49
1:A:1306:A:N6	1:A:1331:G:O2'	2.46	0.49
1:A:381:C:H3'	1:A:382:A:C8	2.48	0.49
1:A:186:C:O2'	20:T:76:ALA:HA	2.12	0.49
1:A:542:G:OP1	4:D:9:LYS:NZ	2.39	0.49
1:A:664:G:O2'	1:A:666:G:OP2	2.29	0.49
2:B:114:LYS:O	2:B:118:THR:HG23	2.12	0.49
1:A:1228:C:P	13:M:106:ARG:HH12	2.30	0.49
13:M:89:ARG:O	13:M:93:GLY:N	2.41	0.49
1:A:109:A:H5'	1:A:110:C:C5	2.48	0.49
1:A:1138:G:H2'	1:A:1140:C:C2	2.48	0.49
1:A:618:C:H42	1:A:623:C:H42	1.61	0.49
1:A:8:A:N6	4:D:205:LYS:HB2	2.28	0.49
6:F:2:ARG:NH1	6:F:68:GLN:HB2	2.28	0.49
13:M:18:LEU:O	13:M:21:ILE:HG12	2.13	0.49
22:V:28:G:C2	22:V:29:G:C4	3.01	0.49
23:W:1:C:N3	23:W:2:G:N1	2.61	0.49
1:A:269:C:H2'	1:A:270:A:C8	2.48	0.49
1:A:382:A:H2'	1:A:383:A:C8	2.47	0.49
1:A:465:A:H4'	1:A:466:A:C6	2.48	0.49
1:A:590:U:O2'	1:A:591:U:H5''	2.12	0.49
21:U:27:VAL:CB	21:U:31:VAL:HG11	2.43	0.49
1:A:1054:C:C2	22:V:34:A:C1'	2.95	0.49
22:V:67:C:C4	22:V:68:C:C5	3.01	0.49
1:A:1370:G:H5''	9:I:110:VAL:HG21	1.95	0.49
1:A:445:G:H2'	1:A:446:G:H8	1.78	0.49
1:A:7:A:H5'	1:A:298:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:23:ALA:O	10:J:27:GLU:HG2	2.12	0.49
16:P:6:LEU:HG	16:P:17:TYR:HB3	1.94	0.49
19:S:25:GLY:N	19:S:27:LYS:NZ	2.60	0.49
19:S:35:ARG:NH2	19:S:71:GLY:O	2.46	0.49
1:A:1190:G:OP1	3:C:4:VAL:N	2.42	0.48
1:A:725:G:OP1	1:A:833:G:N2	2.44	0.48
2:B:186:VAL:O	2:B:200:PRO:HA	2.13	0.48
10:J:84:VAL:HA	10:J:87:LEU:CB	2.43	0.48
1:A:1054:C:O2	1:A:1196:A:N6	2.46	0.48
1:A:460:A:O2'	1:A:461:A:H2'	2.13	0.48
1:A:573:A:H2'	1:A:574:A:C8	2.48	0.48
4:D:58:GLN:O	4:D:62:ARG:HG2	2.13	0.48
5:E:155:LYS:HA	5:E:158:LYS:HB2	1.94	0.48
8:H:17:GLN:NE2	8:H:62:LEU:HD22	2.28	0.48
1:A:1527:U:OP2	21:U:38:GLU:HG3	2.12	0.48
1:A:192:A:H8	1:A:192:A:OP2	1.95	0.48
1:A:719:C:H5''	1:A:720:C:OP2	2.13	0.48
2:B:182:VAL:HG12	2:B:184:ALA:H	1.77	0.48
1:A:932:C:H5'	7:G:3:ARG:HB2	1.96	0.48
9:I:111:GLU:O	9:I:112:ARG:CB	2.61	0.48
12:L:80:LEU:O	12:L:97:VAL:HG12	2.13	0.48
22:V:25:C:C4	22:V:26:A:C8	3.02	0.48
22:V:56:C:C2	22:V:57:G:C5	3.01	0.48
3:C:72:PRO:O	3:C:76:ILE:HG22	2.14	0.48
9:I:94:ARG:HA	9:I:97:LEU:HD12	1.95	0.48
13:M:68:LEU:CD2	13:M:69:ARG:HH12	2.26	0.48
16:P:42:ILE:HG22	16:P:43:ALA:N	2.28	0.48
20:T:12:GLN:O	20:T:16:ALA:N	2.47	0.48
1:A:139:A:H2'	1:A:140:U:O4'	2.14	0.48
1:A:1430:A:H2'	1:A:1431:A:O4'	2.14	0.48
1:A:1441:A:H62	1:A:1461:G:N2	2.11	0.48
1:A:562:U:O2'	12:L:11:ARG:HD3	2.13	0.48
9:I:113:LYS:NZ	9:I:117:LEU:HD22	2.29	0.48
10:J:48:ARG:NH1	14:N:100:TRP:CG	2.80	0.48
22:V:25:C:H2'	22:V:25:C:O2	2.11	0.48
25:O:67:VAL:O	25:O:71:LEU:HG	2.13	0.48
1:A:1291:U:OP1	7:G:36:SER:OG	2.20	0.48
1:A:212:G:OP2	1:A:212:G:H8	1.96	0.48
1:A:580:C:H2'	1:A:581:G:O4'	2.14	0.48
7:G:68:VAL:HG12	7:G:134:VAL:HG12	1.96	0.48
1:A:975:A:O2'	14:N:71:GLY:HA2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:25:GLY:N	19:S:27:LYS:HZ1	2.12	0.48
22:V:33:U:HO2'	22:V:34:A:H2	0.53	0.48
1:A:1463:U:H2'	1:A:1464:U:C6	2.49	0.48
1:A:928:G:O2'	1:A:1533:C:H5'	2.14	0.48
1:A:93:U:H2'	1:A:95:C:C5	2.49	0.48
2:B:89:PHE:CZ	2:B:153:MET:HA	2.49	0.48
14:N:73:LEU:HB2	14:N:78:LEU:HB2	1.96	0.48
27:2:48:ILE:HG21	27:2:57:VAL:HG21	1.95	0.48
1:A:1322:C:P	19:S:77:ARG:HH12	2.37	0.48
1:A:59:A:H5''	1:A:387:U:H4'	1.96	0.48
1:A:417:G:N2	1:A:427:U:O2	2.47	0.48
1:A:462:G:O2'	1:A:463:U:H5''	2.13	0.48
1:A:572:A:H4'	1:A:573:A:OP2	2.13	0.48
13:M:85:TYR:OH	13:M:89:ARG:NE	2.42	0.48
20:T:54:GLN:HB3	20:T:55:PRO:HD3	1.95	0.48
24:X:12:C:P	24:X:12:C:C3'	3.01	0.48
1:A:559:A:H4'	1:A:560:A:H3'	1.94	0.48
1:A:877:G:H2'	1:A:878:A:H8	1.79	0.48
2:B:166:ASP:HA	2:B:190:SER:OG	2.14	0.48
3:C:146:LYS:HB3	3:C:202:PHE:HD2	1.79	0.48
11:K:51:PHE:CD1	11:K:55:ARG:NH1	2.81	0.48
1:A:1516:G:N2	1:A:1519:A:OP2	2.35	0.47
1:A:256:U:H5'	1:A:257:G:OP2	2.13	0.47
1:A:6:G:H2'	1:A:6:G:OP2	2.14	0.47
1:A:80:A:N7	1:A:87:C:N4	2.62	0.47
1:A:831:A:H2'	1:A:832:G:O4'	2.14	0.47
4:D:182:LYS:HZ1	4:D:183:ARG:HH12	1.60	0.47
4:D:94:GLU:OE2	4:D:190:LEU:HD11	2.13	0.47
9:I:47:VAL:O	9:I:50:PRO:HD2	2.14	0.47
22:V:36:G:H2'	22:V:37:A:C8	2.49	0.47
1:A:1117:A:H4'	1:A:1118:U:OP2	2.13	0.47
1:A:299:G:N2	1:A:565:U:O2	2.47	0.47
1:A:321:A:HO2'	1:A:1435:G:HO2'	1.58	0.47
1:A:374:A:C2	16:P:17:TYR:OH	2.65	0.47
1:A:86:G:N2	1:A:87:C:O2	2.48	0.47
2:B:71:THR:OG1	2:B:92:ASN:HA	2.14	0.47
1:A:1195:C:H5''	1:A:1196:A:OP2	2.14	0.47
1:A:1271:A:H2'	1:A:1272:G:C8	2.48	0.47
1:A:1358:U:OP1	14:N:74:ARG:N	2.47	0.47
1:A:407:U:H2'	1:A:408:A:C8	2.49	0.47
4:D:112:GLU:OE2	4:D:153:ARG:NE	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:10:VAL:HG11	6:F:18:VAL:HG22	1.96	0.47
8:H:76:ARG:HG3	8:H:126:CYS:HB3	1.96	0.47
1:A:137:U:O4'	16:P:64:GLY:HA3	2.15	0.47
19:S:10:ILE:HG21	19:S:15:LEU:HD22	1.96	0.47
1:A:1258:G:O6	1:A:1277:C:N4	2.47	0.47
1:A:264:C:H4'	17:Q:64:ARG:NH2	2.28	0.47
1:A:59:A:OP1	1:A:387:U:H5'	2.14	0.47
1:A:408:A:H5''	4:D:7:LYS:HZ1	1.78	0.47
1:A:677:U:H3	1:A:713:G:H22	1.62	0.47
9:I:29:ILE:HG12	9:I:30:ASN:HD22	1.80	0.47
14:N:25:GLU:HB3	14:N:30:ILE:H	1.79	0.47
21:U:23:GLU:O	21:U:24:LYS:HB3	2.14	0.47
1:A:1376:U:H2'	1:A:1377:A:C8	2.50	0.47
1:A:1436:U:H2'	1:A:1437:A:C8	2.50	0.47
3:C:11:LEU:HD13	3:C:17:TRP:NE1	2.30	0.47
4:D:131:ILE:HG22	4:D:133:SER:N	2.28	0.47
12:L:17:LYS:NZ	12:L:19:ASN:ND2	2.62	0.47
22:V:30:G:C6	22:V:40:C:N4	2.83	0.47
22:V:73:A:C2'	22:V:74:C:OP2	2.61	0.47
1:A:1414:U:H2'	1:A:1415:G:H8	1.79	0.47
1:A:14:U:O2	1:A:14:U:C2'	3.34	0.47
1:A:789:U:H2'	1:A:791:G:OP2	2.14	0.47
4:D:97:LEU:HA	4:D:100:VAL:HG22	1.97	0.47
22:V:10:G:N3	22:V:10:G:H2'	2.30	0.47
1:A:1347:G:O2'	1:A:1373:G:O6	2.24	0.47
1:A:516:U:H5''	1:A:517:G:OP2	2.14	0.47
16:P:67:ILE:HG13	16:P:71:VAL:HG12	1.97	0.47
22:V:29:G:C2	22:V:42:C:C2	3.02	0.47
1:A:520:A:OP1	12:L:48:LEU:HB2	2.13	0.47
1:A:649:A:H2'	1:A:650:G:O4'	2.14	0.47
1:A:570:G:O6	1:A:865:A:N6	2.47	0.47
4:D:181:PHE:CZ	4:D:185:PRO:HD3	2.49	0.47
5:E:73:VAL:HG21	5:E:143:LEU:HG	1.96	0.47
1:A:941:G:H22	9:I:125:GLN:CD	2.18	0.47
3:C:24:ASN:HD21	10:J:11:LYS:HZ2	1.62	0.47
16:P:11:ALA:O	16:P:12:LYS:C	2.52	0.47
1:A:1154:G:H2'	1:A:1155:A:C8	2.50	0.47
1:A:292:G:H21	1:A:609:A:H2	1.62	0.47
1:A:375:U:H6	1:A:375:U:OP2	1.98	0.47
22:V:75:C:H6	22:V:75:C:H3'	1.79	0.47
1:A:1070:U:O2	1:A:1106:G:N2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1175:G:H2'	1:A:1176:A:C8	2.49	0.47
1:A:129:A:H8	1:A:129:A:OP2	1.98	0.47
1:A:1441:A:N6	1:A:1462:C:H1'	2.23	0.47
1:A:205:A:H8	1:A:205:A:P	2.38	0.47
1:A:586:C:H2'	1:A:587:G:H5''	1.97	0.47
7:G:132:THR:HA	7:G:135:LYS:HG2	1.97	0.47
18:R:41:SER:OG	18:R:51:GLN:OE1	2.31	0.47
21:U:14:ALA:H	21:U:16:ARG:HH22	1.62	0.47
23:W:21:A:N6	23:W:22:G:O6	2.47	0.47
1:A:1351:U:H2'	1:A:1352:C:C6	2.50	0.47
1:A:149:A:H5'	1:A:1446:A:H1'	1.97	0.47
1:A:211:G:N3	1:A:211:G:H3'	2.30	0.47
1:A:484:G:H1'	1:A:485:U:OP2	2.15	0.47
1:A:71:A:H5''	1:A:72:A:OP2	2.15	0.47
1:A:8:A:H62	4:D:205:LYS:HB2	1.80	0.47
2:B:202:ASN:ND2	2:B:205:ALA:H	2.10	0.47
4:D:169:TRP:CZ3	4:D:189:ASP:HB3	2.49	0.47
16:P:48:GLU:CD	16:P:49:GLY:H	2.17	0.47
1:A:1242:G:H1	1:A:1295:U:H3	1.62	0.46
1:A:1265:C:H2'	1:A:1266:G:C8	2.48	0.46
1:A:1332:A:HO2'	1:A:1333:A:P	2.38	0.46
1:A:373:A:H2'	1:A:373:A:N3	2.30	0.46
1:A:445:G:H2'	1:A:446:G:C8	2.50	0.46
1:A:64:G:H4'	1:A:65:A:H5''	1.97	0.46
1:A:672:U:O2'	6:F:86:ARG:NH1	2.47	0.46
1:A:6:G:H22	5:E:99:SER:HB2	1.79	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.97	0.46
1:A:952:U:H2'	1:A:953:G:C8	2.50	0.46
2:B:202:ASN:HD22	2:B:205:ALA:HB3	1.79	0.46
10:J:14:ASP:HB3	10:J:17:LEU:HB3	1.97	0.46
11:K:109:ILE:HG22	21:U:19:LYS:HE2	1.97	0.46
1:A:280:C:O2'	17:Q:39:ARG:NH1	2.48	0.46
22:V:3:C:N3	22:V:4:C:C5	2.82	0.46
1:A:218:U:OP2	1:A:218:U:H2'	2.16	0.46
1:A:375:U:H5''	16:P:70:ARG:HB3	1.57	0.46
1:A:377:G:O2'	1:A:378:G:H8	1.98	0.46
1:A:407:U:H2'	1:A:408:A:H8	1.79	0.46
1:A:484:G:H4'	1:A:485:U:O5'	2.15	0.46
1:A:667:G:H2'	1:A:668:G:C8	2.48	0.46
9:I:91:GLU:OE2	9:I:94:ARG:HD3	2.16	0.46
1:A:1130:A:H61	1:A:1144:G:H1'	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:G:H2'	1:A:551:U:C6	2.51	0.46
5:E:139:THR:O	5:E:144:GLU:N	2.42	0.46
1:A:1009:U:H2'	1:A:1010:U:C6	2.50	0.46
1:A:111:G:O2'	1:A:389:A:N3	2.30	0.46
1:A:40:C:H42	1:A:403:C:H42	1.63	0.46
1:A:484:G:H4'	1:A:485:U:H3'	1.96	0.46
5:E:100:GLU:N	5:E:100:GLU:OE1	2.48	0.46
18:R:49:LYS:O	18:R:52:ARG:HB2	2.15	0.46
11:K:121:ARG:NE	21:U:34:ARG:HH11	2.14	0.46
22:V:34:A:N3	22:V:34:A:H3'	2.30	0.46
5:E:67:ARG:HH21	5:E:68:ARG:HH12	1.63	0.46
14:N:5:MET:HG2	14:N:8:ARG:HH21	1.79	0.46
22:V:50:U:H2'	22:V:51:U:O4'	2.15	0.46
1:A:1030:U:H5'	1:A:1031:C:C4	2.50	0.46
1:A:1075:U:H2'	1:A:1076:U:H6	1.81	0.46
1:A:1301:U:O2'	1:A:1302:C:O5'	2.30	0.46
1:A:167:A:H2'	1:A:168:G:C8	2.50	0.46
1:A:236:A:H2'	1:A:237:G:H8	1.79	0.46
10:J:21:ALA:HA	10:J:24:GLU:HG2	1.98	0.46
10:J:63:ASP:OD2	10:J:65:TYR:CE2	2.69	0.46
13:M:69:ARG:HA	13:M:72:ILE:HG22	1.96	0.46
19:S:62:THR:HB	19:S:65:MET:HG3	1.97	0.46
21:U:27:VAL:HG13	21:U:31:VAL:HG11	1.94	0.46
31:7:26:HIS:NE2	31:7:48:ALA:HB2	2.31	0.46
1:A:1279:G:H2'	1:A:1279:G:N3	2.30	0.46
1:A:736:C:H5''	6:F:90:MET:SD	2.55	0.46
3:C:22:PHE:HZ	10:J:11:LYS:HZ3	1.56	0.46
4:D:58:GLN:HA	4:D:61:ARG:HG2	1.97	0.46
4:D:74:TYR:HD1	4:D:92:LEU:HB3	1.80	0.46
16:P:42:ILE:O	16:P:43:ALA:HB3	2.16	0.46
11:K:88:PRO:HB3	21:U:28:LEU:HD23	1.97	0.46
1:A:1095:U:H2'	1:A:1096:C:C6	2.50	0.46
1:A:1447:A:H5'	1:A:1448:C:H5	1.81	0.46
1:A:796:C:OP1	11:K:126:ARG:HA	2.16	0.46
7:G:70:PRO:O	7:G:95:ARG:HG2	2.15	0.46
10:J:53:ILE:HG22	10:J:61:ALA:O	2.16	0.46
16:P:75:ILE:C	16:P:77:GLU:H	2.18	0.46
1:A:1254:A:H2'	1:A:1255:G:H8	1.81	0.46
1:A:375:U:H4'	16:P:6:LEU:HB3	1.98	0.46
1:A:75:G:H2'	1:A:76:G:H8	1.81	0.46
1:A:793:U:H3'	1:A:794:A:H5''	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:A:H2'	1:A:81:A:C8	2.51	0.46
2:B:203:ASP:OD1	2:B:204:ASP:N	2.48	0.46
3:C:54:ILE:HD13	3:C:67:ILE:HD13	1.97	0.46
15:O:9:LYS:O	15:O:13:GLU:HG3	2.15	0.46
22:V:10:G:C2	22:V:11:C:C5	3.04	0.46
1:A:1073:U:C4	1:A:1074:G:N7	2.84	0.46
1:A:275:G:C2	1:A:276:G:C4	3.03	0.46
2:B:212:TYR:O	2:B:216:VAL:HG23	2.15	0.46
3:C:180:ASP:OD2	3:C:203:LYS:HB3	2.17	0.46
9:I:90:ASP:OD2	9:I:93:LEU:HG	2.16	0.46
14:N:14:ALA:O	14:N:18:LYS:HG3	2.16	0.46
3:C:39:ARG:NH2	14:N:91:GLU:OE2	2.49	0.46
22:V:68:C:N3	22:V:69:G:C8	2.84	0.46
9:I:129:ARG:CA	23:W:32:A:OP1	2.62	0.46
1:A:378:G:N2	1:A:386:C:O2	2.49	0.45
1:A:438:U:H4'	4:D:119:HIS:CD2	2.51	0.45
1:A:457:G:H21	1:A:476:U:H2'	1.79	0.45
1:A:641:U:O2'	1:A:642:A:OP2	2.28	0.45
2:B:45:THR:HB	2:B:49:PHE:HE2	1.80	0.45
4:D:84:ASN:HD22	4:D:87:GLU:HB2	1.80	0.45
22:V:27:G:N3	22:V:28:G:N7	2.64	0.45
22:V:40:C:O2	22:V:41:C:C5	2.69	0.45
28:3:25:VAL:CG1	28:3:26:THR:N	2.80	0.45
1:A:1149:C:H2'	1:A:1150:A:C8	2.52	0.45
1:A:944:G:H2'	1:A:1338:G:H22	1.81	0.45
3:C:156:LEU:HD22	3:C:165:GLU:OE2	2.16	0.45
3:C:35:ASP:OD1	3:C:58:ARG:NH1	2.49	0.45
17:Q:17:GLU:OE2	17:Q:18:LYS:NZ	2.49	0.45
20:T:27:MET:O	20:T:31:ILE:HG22	2.16	0.45
22:V:2:C:C2	22:V:3:C:C5	3.05	0.45
30:6:44:VAL:HG13	30:6:45:SER:H	1.81	0.45
1:A:1019:A:H5''	1:A:1020:G:OP2	2.16	0.45
11:K:80:ASN:OD1	11:K:105:ARG:NH2	2.50	0.45
13:M:67:ASP:HA	13:M:70:ARG:HD2	1.98	0.45
21:U:3:ILE:HG13	21:U:5:VAL:HG23	1.98	0.45
22:V:41:C:N3	22:V:42:C:C6	2.85	0.45
1:A:100:G:H3'	1:A:100:G:N3	2.31	0.45
3:C:154:GLY:H	3:C:164:THR:H	1.63	0.45
4:D:112:GLU:O	4:D:115:GLN:HB3	2.16	0.45
5:E:71:ILE:HD13	5:E:144:GLU:HB2	1.98	0.45
1:A:1348:U:OP2	9:I:111:GLU:CB	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:U:P	11:K:86:LYS:NZ	2.89	0.45
1:A:932:C:P	7:G:3:ARG:HH21	2.39	0.45
8:H:105:THR:OG1	8:H:108:GLY:O	2.32	0.45
13:M:68:LEU:HG	13:M:69:ARG:NH1	2.32	0.45
16:P:10:GLY:O	16:P:11:ALA:CB	2.64	0.45
22:V:75:C:O2'	22:V:76:A:P	2.75	0.45
23:W:72:G:C3'	23:W:73:A:C5'	2.91	0.45
24:X:17:C:O2	24:X:17:C:H2'	2.16	0.45
1:A:860:A:H61	1:A:872:A:H62	1.65	0.45
5:E:50:GLY:HA3	5:E:61:LYS:HB2	1.99	0.45
8:H:86:LYS:HD2	8:H:90:GLU:HB3	1.99	0.45
27:2:5:ILE:HG21	27:2:57:VAL:HG13	1.99	0.45
2:B:165:ALA:HB3	2:B:186:VAL:HG12	1.97	0.45
4:D:12:ARG:NH2	4:D:36:ALA:H	2.14	0.45
5:E:82:HIS:HE1	8:H:95:MET:HG3	1.82	0.45
1:A:1013:G:P	19:S:17:LYS:NZ	2.90	0.45
1:A:1234:C:H1'	1:A:1364:U:C6	2.52	0.45
1:A:1427:C:H42	1:A:1473:G:H1	1.63	0.45
1:A:1436:U:H2'	1:A:1437:A:H8	1.80	0.45
1:A:386:C:H3'	1:A:387:U:C6	2.51	0.45
1:A:923:A:OP1	5:E:25:LYS:HE2	2.17	0.45
5:E:96:GLN:HA	5:E:97:PRO:HD3	1.81	0.45
1:A:526:C:OP2	12:L:87:LYS:HE3	2.17	0.45
16:P:16:PHE:O	16:P:16:PHE:CD1	2.70	0.45
1:A:1314:C:OP2	19:S:5:LYS:HG3	2.17	0.45
13:M:84:CYS:SG	19:S:72:GLU:OE2	2.75	0.45
1:A:1118:U:OP2	9:I:105:ARG:CZ	2.65	0.45
1:A:1202:U:H2'	1:A:1203:C:O4'	2.15	0.45
1:A:75:G:H2'	1:A:76:G:C8	2.52	0.45
2:B:53:LEU:HA	2:B:219:THR:HG23	1.99	0.45
3:C:166:TRP:CH2	3:C:168:ARG:NH1	2.85	0.45
12:L:56:LEU:HB2	12:L:59:GLY:O	2.17	0.45
1:A:1202:U:C2	14:N:81:ILE:HD11	2.52	0.45
19:S:38:THR:HA	19:S:69:LYS:HA	1.99	0.45
22:V:26:A:C6	22:V:27:G:C5	3.04	0.45
22:V:28:G:C2	22:V:29:G:N9	2.85	0.45
1:A:1339:A:C2	23:W:41:C:O2	2.69	0.45
1:A:45:G:H2'	1:A:46:G:C8	2.52	0.45
1:A:683:G:H21	11:K:39:ASN:ND2	2.14	0.45
4:D:106:PHE:HD1	4:D:158:LEU:HD21	1.82	0.45
8:H:12:ARG:HH11	8:H:26:MET:CB	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:42:LEU:HD11	10:J:73:LEU:HD13	1.99	0.45
17:Q:14:ASP:OD2	17:Q:54:ILE:N	2.50	0.45
21:U:7:GLU:HG3	21:U:10:PRO:HA	1.99	0.45
22:V:18:G:H5''	22:V:18:G:C8	2.51	0.45
1:A:1526:G:C6	1:A:1527:U:O4	2.70	0.44
1:A:188:C:O2	1:A:188:C:H2'	2.17	0.44
1:A:508:U:H5''	4:D:50:TYR:CD2	2.52	0.44
4:D:60:VAL:HA	4:D:63:ILE:HG22	1.99	0.44
18:R:62:ARG:HD2	18:R:69:TYR:HA	1.98	0.44
19:S:44:ILE:HG21	19:S:63:ASP:OD1	2.17	0.44
1:A:1004:A:H2'	1:A:1005:A:O4'	2.17	0.44
1:A:1138:G:H3'	1:A:1138:G:N3	2.33	0.44
1:A:1187:G:H4'	9:I:114:LYS:HZ3	1.81	0.44
1:A:130:A:H1'	1:A:264:C:O4'	2.18	0.44
1:A:1382:C:H2'	1:A:1383:C:H6	1.82	0.44
1:A:148:G:HO2'	1:A:149:A:P	2.37	0.44
1:A:695:A:O2'	1:A:696:A:H8	2.01	0.44
1:A:707:U:OP1	11:K:86:LYS:NZ	2.42	0.44
15:O:24:THR:HG21	15:O:69:LEU:HD21	1.98	0.44
19:S:24:SER:HB3	19:S:27:LYS:HZ1	1.81	0.44
1:A:1401:G:C6	1:A:1402:C:C2	3.05	0.44
1:A:97:G:H3'	1:A:98:A:H8	1.83	0.44
3:C:106:ARG:HH21	3:C:111:ASP:HB3	1.83	0.44
4:D:100:VAL:HG11	4:D:136:VAL:HG21	1.98	0.44
11:K:121:ARG:HE	21:U:34:ARG:HH11	1.64	0.44
14:N:41:TRP:O	14:N:44:VAL:HG12	2.18	0.44
16:P:37:GLY:HA2	16:P:51:ARG:HH11	1.82	0.44
1:A:236:A:H5'	17:Q:43:LEU:HD12	1.99	0.44
22:V:75:C:H2'	22:V:76:A:N9	2.33	0.44
1:A:301:G:H4'	1:A:302:G:OP1	2.16	0.44
1:A:694:A:H2'	1:A:695:A:H5'	2.00	0.44
9:I:87:MET:HB2	9:I:94:ARG:HD2	2.00	0.44
1:A:1319:A:C5'	19:S:69:LYS:HZ3	2.30	0.44
22:V:49:C:H2'	22:V:49:C:O2	2.16	0.44
22:V:3:C:C2	22:V:4:C:C5	3.06	0.44
1:A:366:A:H1'	1:A:395:C:O2	2.17	0.44
1:A:823:C:H42	1:A:877:G:H1	1.64	0.44
13:M:111:PRO:HD2	13:M:113:LYS:HZ1	1.83	0.44
18:R:25:ILE:O	18:R:29:LYS:HG2	2.17	0.44
1:A:1232:U:OP2	9:I:128:LYS:HE3	2.18	0.44
1:A:1281:C:H5''	1:A:1282:C:H5	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:G:H2'	1:A:36:C:O4'	2.18	0.44
1:A:443:C:H2'	1:A:444:G:H8	1.82	0.44
1:A:652:U:O2'	1:A:752:G:N1	2.44	0.44
1:A:784:A:H2'	1:A:785:G:O4'	2.18	0.44
4:D:74:TYR:CD1	4:D:92:LEU:HB3	2.53	0.44
9:I:128:LYS:O	23:W:32:A:OP1	2.36	0.44
9:I:8:THR:O	9:I:81:GLY:HA2	2.18	0.44
28:3:29:SER:HG	28:3:40:ARG:CD	2.10	0.44
1:A:1164:G:H2'	1:A:1165:U:C6	2.53	0.44
1:A:1219:A:H2'	1:A:1220:G:H8	1.82	0.44
1:A:377:G:OP2	1:A:377:G:H4'	2.18	0.44
1:A:475:C:H2'	1:A:476:U:C5	2.52	0.44
1:A:1152:A:P	10:J:72:ARG:HH22	2.41	0.44
12:L:95:HIS:HB3	12:L:96:THR:H	1.67	0.44
15:O:23:SER:HB2	15:O:26:VAL:HG23	2.00	0.44
26:1:11:VAL:O	26:1:15:ASN:ND2	2.51	0.44
1:A:1293:C:H2'	1:A:1294:G:H8	1.83	0.44
2:B:113:LEU:HD13	2:B:143:LEU:HB3	1.98	0.44
11:K:51:PHE:HD1	11:K:55:ARG:HB3	1.81	0.44
1:A:1216:A:H5''	14:N:4:SER:OG	2.18	0.44
1:A:713:G:H2'	1:A:714:G:C8	2.53	0.44
1:A:815:A:N7	1:A:1509:C:O2'	2.48	0.44
2:B:183:PHE:CD1	2:B:197:PHE:HD2	2.36	0.44
7:G:30:MET:HG3	7:G:34:LYS:O	2.18	0.44
10:J:21:ALA:HA	10:J:24:GLU:OE2	2.18	0.44
12:L:30:ARG:O	12:L:57:THR:HG23	2.17	0.44
16:P:10:GLY:HA2	16:P:16:PHE:HB3	2.00	0.44
21:U:28:LEU:HD12	21:U:28:LEU:N	2.32	0.44
1:A:1252:A:H61	1:A:1285:A:N6	2.14	0.43
1:A:1341:U:OP1	23:W:32:A:H5''	2.18	0.43
1:A:444:G:C6	1:A:491:G:C6	3.06	0.43
1:A:680:C:H2'	1:A:681:A:C8	2.53	0.43
1:A:946:A:H2'	1:A:947:G:H8	1.83	0.43
2:B:113:LEU:HD13	2:B:143:LEU:CB	2.48	0.43
4:D:44:LYS:HD2	4:D:45:PRO:HD2	1.99	0.43
13:M:111:PRO:O	13:M:113:LYS:HG3	2.18	0.43
18:R:32:ILE:HD13	18:R:67:LEU:HD13	1.99	0.43
22:V:53:G:N2	22:V:62:C:C2	2.85	0.43
1:A:1249:C:OP1	9:I:32:ARG:NH2	2.51	0.43
1:A:1300:G:O2'	1:A:1301:U:P	2.76	0.43
1:A:367:U:O4'	1:A:394:G:N2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:G:H21	5:E:102:THR:HG21	1.83	0.43
1:A:723:U:H5'	1:A:724:G:H5''	1.99	0.43
4:D:12:ARG:NH1	4:D:37:PRO:HA	2.32	0.43
5:E:145:ASN:O	5:E:146:MET:HG2	2.18	0.43
16:P:17:TYR:CD1	16:P:17:TYR:N	2.86	0.43
22:V:40:C:C2	22:V:41:C:C5	3.06	0.43
22:V:56:C:N3	22:V:57:G:N1	2.65	0.43
22:V:19:G:C2	22:V:57:G:N2	2.85	0.43
24:X:15:G:H2'	24:X:16:C:C5'	2.48	0.43
1:A:1002:G:H1	1:A:1038:C:H42	1.65	0.43
1:A:1451:U:OP2	1:A:1452:C:C5	2.71	0.43
1:A:219:U:H2'	1:A:220:G:C8	2.52	0.43
1:A:387:U:O5'	1:A:387:U:H6	2.01	0.43
1:A:628:G:H2'	1:A:629:A:C8	2.52	0.43
2:B:159:ALA:HB1	2:B:183:PHE:HE2	1.83	0.43
3:C:107:LYS:NZ	3:C:143:LEU:O	2.37	0.43
5:E:139:THR:HA	5:E:143:LEU:HB2	1.99	0.43
16:P:67:ILE:HG23	16:P:72:ALA:HB2	1.99	0.43
21:U:35:GLU:HB3	21:U:39:LYS:HB2	2.00	0.43
1:A:1178:G:C8	9:I:98:ARG:NH1	2.77	0.43
1:A:1292:G:H5''	9:I:40:ARG:NH1	2.33	0.43
1:A:163:C:H2'	1:A:164:G:O4'	2.17	0.43
1:A:315:A:H4'	1:A:353:A:H62	1.83	0.43
1:A:374:A:C8	1:A:375:U:C4	3.07	0.43
1:A:573:A:N3	1:A:883:C:O2'	2.52	0.43
1:A:652:U:HO2'	1:A:752:G:N2	2.17	0.43
1:A:863:U:H2'	1:A:865:A:OP2	2.18	0.43
23:W:34:G:O2'	23:W:35:C:C6	2.68	0.43
1:A:1477:U:H2'	1:A:1478:U:C6	2.53	0.43
1:A:373:A:H62	1:A:481:G:C4'	2.31	0.43
1:A:692:U:O2'	1:A:694:A:N7	2.40	0.43
1:A:787:A:H2'	1:A:788:U:C6	2.53	0.43
1:A:83:C:O2'	1:A:85:U:OP2	2.37	0.43
2:B:67:LEU:HD11	2:B:91:VAL:HG23	1.99	0.43
16:P:46:LYS:HB2	16:P:47:GLU:H	1.60	0.43
23:W:49:G:H3'	23:W:50:G:C8	2.53	0.43
1:A:1130:A:N6	1:A:1144:G:H1'	2.33	0.43
1:A:447:G:N2	1:A:487:A:H62	2.17	0.43
1:A:85:U:H4'	1:A:86:G:O4'	2.18	0.43
7:G:69:ARG:HB2	7:G:95:ARG:HB3	2.01	0.43
10:J:15:HIS:HA	10:J:18:ILE:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:5:ARG:NH1	10:J:79:PRO:HD2	2.33	0.43
19:S:44:ILE:HD13	19:S:63:ASP:OD1	2.19	0.43
22:V:75:C:H4'	22:V:76:A:OP1	2.18	0.43
28:3:25:VAL:CG1	28:3:26:THR:H	2.31	0.43
1:A:429:U:O2'	4:D:21:LYS:NZ	2.41	0.43
2:B:22:TRP:HA	2:B:188:THR:HG22	2.00	0.43
3:C:149:LYS:HD2	3:C:166:TRP:HE1	1.83	0.43
3:C:40:GLN:O	3:C:44:LYS:HG2	2.19	0.43
4:D:84:ASN:OD1	5:E:101:GLY:HA3	2.19	0.43
6:F:75:GLU:OE2	6:F:79:ARG:NE	2.51	0.43
3:C:24:ASN:ND2	10:J:11:LYS:NZ	2.66	0.43
15:O:81:ILE:HG23	15:O:86:LEU:O	2.19	0.43
22:V:58:A:O2'	22:V:61:C:N4	2.52	0.43
1:A:1239:A:N6	1:A:1299:A:H62	2.16	0.43
1:A:1257:A:C2	14:N:20:PHE:HE2	2.36	0.43
1:A:26:A:N6	1:A:558:G:H1'	2.34	0.43
1:A:377:G:H2'	1:A:378:G:H5''	2.01	0.43
1:A:710:G:H2'	1:A:711:G:C8	2.54	0.43
1:A:787:A:H2'	1:A:788:U:H6	1.83	0.43
2:B:96:LEU:H	2:B:99:MET:HE3	1.83	0.43
5:E:11:GLN:HE21	5:E:116:VAL:HG12	1.84	0.43
9:I:122:ARG:HG2	9:I:123:ARG:N	2.32	0.43
16:P:33:ILE:O	16:P:34:GLU:HB3	2.18	0.43
1:A:1296:C:N4	1:A:1297:G:O6	2.51	0.43
1:A:248:C:H4'	1:A:283:U:O2'	2.19	0.43
1:A:357:G:OP1	1:A:367:U:H2'	2.19	0.43
1:A:96:U:H2'	1:A:97:G:H8	1.82	0.43
3:C:149:LYS:NZ	3:C:200:TRP:CE2	2.86	0.43
10:J:45:ARG:HG3	10:J:47:GLU:OE2	2.19	0.43
17:Q:51:GLU:OE1	17:Q:51:GLU:N	2.51	0.43
20:T:70:LYS:HG3	20:T:73:ARG:NH2	2.31	0.43
23:W:49:G:O2'	23:W:50:G:OP1	2.31	0.43
28:3:43:ILE:HG22	28:3:49:TYR:HB2	2.01	0.43
1:A:1252:A:O2'	1:A:1369:C:H4'	2.19	0.43
1:A:1308:U:H2'	1:A:1309:G:C8	2.44	0.43
1:A:151:A:O2'	1:A:152:A:O5'	2.36	0.43
1:A:235:C:H2'	1:A:236:A:C8	2.54	0.43
1:A:28:A:O2'	1:A:296:U:OP1	2.32	0.43
1:A:411:A:H2'	4:D:30:LYS:HD3	2.01	0.43
1:A:439:U:H5'	4:D:119:HIS:CD2	2.53	0.43
3:C:152:VAL:HG22	3:C:197:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:44:ARG:HA	5:E:71:ILE:O	2.19	0.43
8:H:112:ASP:OD1	8:H:113:ARG:N	2.51	0.43
1:A:942:G:C5	9:I:125:GLN:NE2	2.87	0.43
11:K:93:GLU:OE1	11:K:93:GLU:N	2.45	0.43
19:S:23:GLU:HG2	19:S:24:SER:H	1.83	0.43
1:A:159:G:N2	1:A:162:A:N7	2.67	0.42
1:A:426:U:OP1	4:D:35:GLN:NE2	2.51	0.42
1:A:5:U:C2	1:A:6:G:C8	8.51	0.42
2:B:114:LYS:O	2:B:117:GLU:HB3	2.19	0.42
3:C:146:LYS:HB3	3:C:202:PHE:CD2	2.54	0.42
16:P:71:VAL:O	16:P:75:ILE:HG13	2.18	0.42
20:T:34:VAL:HG21	20:T:53:MET:SD	2.58	0.42
18:R:72:ARG:HG2	21:U:4:LYS:HD3	2.00	0.42
1:A:109:A:C2	1:A:110:C:H1'	8.48	0.42
1:A:1161:C:N4	1:A:1175:G:H1	2.15	0.42
1:A:329:A:N7	1:A:332:G:N1	2.67	0.42
1:A:42:G:N2	1:A:401:C:O2	2.52	0.42
1:A:618:C:N4	1:A:623:C:H42	2.17	0.42
4:D:158:LEU:O	4:D:162:GLU:HG3	2.19	0.42
8:H:48:PHE:HB2	8:H:58:LEU:HD11	2.00	0.42
10:J:56:HIS:CE1	10:J:57:VAL:HG13	2.55	0.42
12:L:32:VAL:HB	12:L:55:ARG:HB3	2.01	0.42
31:7:45:ARG:N	31:7:46:PRO:HD2	2.34	0.42
1:A:1031:C:H4'	1:A:1032:G:C4	2.55	0.42
1:A:409:U:H2'	1:A:410:G:O4'	2.18	0.42
1:A:562:U:H2'	12:L:12:ALA:O	2.18	0.42
1:A:79:G:O6	1:A:91:U:H1'	2.19	0.42
4:D:106:PHE:CD1	4:D:158:LEU:HD21	2.54	0.42
6:F:3:HIS:CE1	6:F:95:ALA:HA	2.54	0.42
9:I:95:SER:O	9:I:99:LYS:HG3	2.19	0.42
1:A:683:G:H21	11:K:39:ASN:HD22	1.65	0.42
1:A:60:A:N6	1:A:110:C:H42	2.17	0.42
1:A:1429:A:H61	1:A:1471:U:H3	1.67	0.42
1:A:415:A:H3'	1:A:416:G:H8	1.84	0.42
5:E:133:ILE:O	5:E:136:VAL:HG22	2.19	0.42
7:G:66:GLU:HG2	7:G:69:ARG:NH2	2.33	0.42
9:I:98:ARG:HE	9:I:103:VAL:CG1	2.32	0.42
11:K:19:VAL:HG13	11:K:82:GLU:O	2.20	0.42
11:K:45:THR:HG23	11:K:48:GLY:N	2.33	0.42
14:N:72:PHE:CE2	14:N:74:ARG:HA	2.55	0.42
11:K:125:LYS:HG2	21:U:33:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:U:H1'	1:A:1179:A:C4	2.54	0.42
1:A:1467:C:H2'	1:A:1468:A:H8	1.85	0.42
2:B:218:ALA:O	2:B:222:GLU:HG2	2.19	0.42
11:K:96:ILE:HA	11:K:99:LEU:HD12	2.02	0.42
21:U:46:ARG:HG2	21:U:50:SER:HG	1.84	0.42
1:A:109:A:C6	1:A:327:A:C6	3.08	0.42
1:A:744:C:H2'	1:A:745:G:C8	2.55	0.42
4:D:123:MET:CE	4:D:145:ARG:HA	2.50	0.42
16:P:20:VAL:HG22	16:P:32:PHE:HB2	2.01	0.42
29:4:11:LEU:HA	29:4:50:LYS:O	2.20	0.42
1:A:1149:C:H2'	1:A:1150:A:H8	1.85	0.42
1:A:1492:A:H2'	1:A:1492:A:N3	2.35	0.42
1:A:950:U:O4	13:M:103:THR:HG21	2.19	0.42
4:D:33:ILE:HG12	4:D:34:GLU:H	1.84	0.42
1:A:1347:G:O3'	9:I:111:GLU:CG	2.68	0.42
10:J:7:ARG:O	10:J:101:SER:N	2.50	0.42
1:A:952:U:C4	13:M:102:LYS:HE3	2.55	0.42
15:O:25:GLU:HA	15:O:80:LEU:HD21	2.01	0.42
16:P:48:GLU:CG	16:P:49:GLY:N	2.82	0.42
22:V:66:U:N3	22:V:67:C:C5	2.87	0.42
1:A:35:G:H21	12:L:114:SER:HB3	1.85	0.42
1:A:402:G:H2'	1:A:403:C:C6	2.55	0.42
3:C:10:ARG:HB3	3:C:14:VAL:HG23	2.01	0.42
6:F:21:MET:HB3	6:F:25:TYR:CE2	2.52	0.42
8:H:77:VAL:HG21	8:H:127:TYR:CD2	2.55	0.42
9:I:17:ARG:HB2	9:I:65:THR:OG1	2.20	0.42
3:C:39:ARG:NE	14:N:91:GLU:OE2	2.52	0.42
22:V:40:C:O2'	22:V:41:C:O4'	2.28	0.42
29:4:50:LYS:O	29:4:51:GLU:HB3	2.19	0.42
3:C:62:SER:HA	3:C:96:VAL:HB	2.02	0.42
4:D:98:ASP:OD2	4:D:110:ARG:NH1	2.51	0.42
1:A:1226:C:H2'	13:M:101:THR:HB	2.02	0.42
1:A:750:C:O2'	15:O:20:ASP:O	2.37	0.42
1:A:1213:A:N7	1:A:1215:G:C6	2.88	0.42
1:A:1258:G:H2'	1:A:1259:C:C6	2.55	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.19	0.42
1:A:186:C:H42	1:A:191:G:H1	1.66	0.42
1:A:299:G:C6	1:A:300:A:C6	3.08	0.42
1:A:407:U:O4	1:A:408:A:N6	2.53	0.42
1:A:446:G:C5	1:A:447:G:C5	3.08	0.42
1:A:468:A:H5''	1:A:469:C:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:A:N6	1:A:622:A:N1	2.68	0.42
1:A:692:U:H2'	1:A:694:A:OP2	2.19	0.42
7:G:21:LEU:HD13	7:G:65:LEU:HD23	2.00	0.42
1:A:1002:G:H1'	1:A:1039:G:N2	2.35	0.41
1:A:1146:A:C6	1:A:1147:C:C2	3.08	0.41
1:A:1158:C:H5''	1:A:1159:U:OP2	2.20	0.41
1:A:187:G:H3'	1:A:189:A:OP2	2.20	0.41
1:A:482:A:N3	1:A:482:A:H2'	2.35	0.41
1:A:5:U:C4'	1:A:6:G:OP2	2.67	0.41
9:I:80:HIS:CE1	9:I:84:ARG:HH21	2.38	0.41
10:J:53:ILE:HG13	14:N:84:ARG:NE	2.35	0.41
14:N:32:ASP:O	14:N:40:ARG:HD3	2.20	0.41
16:P:70:ARG:HG3	16:P:70:ARG:O	2.20	0.41
22:V:24:G:N1	22:V:25:C:C2	2.88	0.41
1:A:1073:U:N3	1:A:1074:G:N7	2.68	0.41
1:A:1346:A:H4'	1:A:1348:U:OP1	2.20	0.41
1:A:374:A:N3	1:A:451:A:OP2	2.53	0.41
5:E:48:GLY:HA3	5:E:65:LYS:HB2	2.02	0.41
6:F:38:ARG:HD2	6:F:40:GLU:OE2	2.20	0.41
12:L:39:THR:HG23	12:L:89:LEU:HD22	2.02	0.41
22:V:37:A:C2	22:V:38:A:O4'	2.73	0.41
1:A:1061:G:H5'	10:J:61:ALA:HB2	2.02	0.41
1:A:1146:A:H2'	1:A:1147:C:O4'	2.20	0.41
1:A:255:G:N2	1:A:272:C:C2	2.88	0.41
4:D:70:GLN:O	4:D:74:TYR:HD2	2.04	0.41
10:J:46:LYS:HZ2	10:J:48:ARG:HE	1.68	0.41
1:A:976:G:N1	1:A:1362:A:O2'	2.22	0.41
1:A:136:C:O4'	16:P:1:MET:CG	2.61	0.41
1:A:119:A:O2'	1:A:240:G:N7	2.45	0.41
1:A:276:G:C6	1:A:277:C:N4	2.88	0.41
1:A:562:U:H5''	1:A:563:A:OP1	2.20	0.41
1:A:94:G:O2'	1:A:95:C:O5'	2.38	0.41
1:A:985:C:H6	1:A:985:C:OP2	2.04	0.41
2:B:81:ASP:OD1	2:B:82:ALA:N	2.53	0.41
6:F:2:ARG:HG3	6:F:91:ARG:HH21	1.84	0.41
7:G:59:GLU:O	7:G:63:VAL:HG23	2.21	0.41
7:G:69:ARG:HB3	7:G:99:ALA:HB2	2.02	0.41
8:H:94:VAL:HG11	8:H:127:TYR:CD2	2.55	0.41
17:Q:24:ILE:HG13	17:Q:41:THR:HB	2.01	0.41
20:T:16:ALA:O	20:T:19:HIS:HB3	2.19	0.41
1:A:263:A:OP1	20:T:73:ARG:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:38:A:C2'	22:V:39:U:H6	2.22	0.41
23:W:3:G:N2	23:W:70:C:C2	2.88	0.41
1:A:764:C:H5'	15:O:49:HIS:CE1	2.55	0.41
2:B:27:LYS:N	2:B:28:PRO:HD2	2.35	0.41
4:D:84:ASN:HD22	4:D:187:ARG:HH22	1.68	0.41
4:D:2:ARG:NH2	4:D:114:ARG:HD2	2.36	0.41
9:I:18:VAL:HG11	9:I:82:ILE:HD13	2.03	0.41
11:K:16:SER:O	11:K:79:LYS:N	2.46	0.41
12:L:4:ASN:HD21	17:Q:35:LYS:HE2	1.84	0.41
15:O:2:LEU:HB2	15:O:34:GLN:NE2	2.36	0.41
1:A:1219:A:H2'	1:A:1220:G:C8	2.56	0.41
5:E:132:PRO:O	5:E:136:VAL:HG13	2.20	0.41
9:I:60:LEU:HD12	9:I:60:LEU:O	2.20	0.41
1:A:944:G:C6	1:A:1338:G:OP2	2.74	0.41
1:A:445:G:H1	1:A:489:C:N4	2.09	0.41
1:A:530:G:N3	1:A:530:G:H2'	2.36	0.41
1:A:637:C:OP2	17:Q:3:LYS:HD3	2.19	0.41
1:A:651:C:N4	1:A:752:G:O2'	2.53	0.41
1:A:707:U:H2'	1:A:708:C:C6	2.55	0.41
1:A:1377:A:C6	7:G:6:ILE:HD13	2.56	0.41
9:I:7:GLY:HA3	9:I:85:ALA:HB2	2.01	0.41
10:J:46:LYS:HE2	10:J:66:GLU:OE1	2.20	0.41
1:A:1005:A:C5	1:A:1006:G:H1'	2.56	0.41
1:A:1367:C:H5'	10:J:62:ARG:HH12	1.80	0.41
1:A:157:U:H1'	1:A:165:G:N2	2.35	0.41
1:A:381:C:H5'	1:A:382:A:OP2	2.20	0.41
1:A:391:G:O2'	1:A:392:C:O4'	2.36	0.41
1:A:630:A:H2'	1:A:631:C:C6	2.55	0.41
3:C:185:THR:HA	3:C:197:VAL:O	2.21	0.41
6:F:21:MET:O	6:F:25:TYR:HD2	2.03	0.41
9:I:91:GLU:CD	9:I:94:ARG:HD3	2.41	0.41
22:V:58:A:HO2'	22:V:59:U:P	2.44	0.41
22:V:65:G:C2	22:V:66:U:C6	3.08	0.41
1:A:236:A:H8	1:A:236:A:OP2	2.03	0.41
1:A:309:A:N6	1:A:310:G:O6	2.54	0.41
1:A:563:A:H5'	1:A:566:G:N2	2.36	0.41
1:A:64:G:N3	1:A:67:C:N4	2.69	0.41
1:A:719:C:O2'	18:R:37:LYS:HB3	2.21	0.41
1:A:765:G:O6	1:A:812:G:O2'	2.35	0.41
4:D:182:LYS:HZ1	4:D:183:ARG:NH1	2.13	0.41
8:H:6:ILE:HD11	8:H:31:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:112:ARG:HG2	9:I:113:LYS:N	2.36	0.41
1:A:230:G:H3'	16:P:31:ARG:HH22	1.85	0.41
1:A:1220:G:N2	19:S:53:GLY:O	2.52	0.41
19:S:33:TRP:CE2	19:S:56:HIS:HE1	2.39	0.41
21:U:47:ALA:O	21:U:50:SER:HB2	2.20	0.41
22:V:39:U:O2'	22:V:40:C:P	2.79	0.41
22:V:40:C:C2	22:V:41:C:C6	3.09	0.41
22:V:74:C:O2'	22:V:75:C:P	2.78	0.41
1:A:363:A:OP2	12:L:57:THR:HG21	2.21	0.41
1:A:456:A:N6	1:A:457:G:O6	2.54	0.41
1:A:923:A:N6	1:A:1392:G:O6	2.54	0.41
2:B:20:ARG:HH21	2:B:21:TYR:HE1	1.68	0.41
3:C:128:MET:HB2	3:C:132:ALA:HB2	2.03	0.41
7:G:56:SER:O	7:G:60:ALA:HB2	2.21	0.41
11:K:89:GLY:HA2	11:K:90:PRO:HD3	1.90	0.41
22:V:75:C:C3'	22:V:75:C:C6	3.03	0.41
22:V:74:C:O2'	22:V:75:C:H5'	2.21	0.41
23:W:9:A:C2	23:W:45:G:C6	3.08	0.41
1:A:1145:A:H4'	1:A:1146:A:H5''	2.03	0.41
1:A:1258:G:H2'	1:A:1259:C:H6	1.86	0.41
1:A:268:U:H2'	1:A:269:C:C6	2.56	0.41
1:A:389:A:H8	1:A:390:U:C6	2.39	0.41
1:A:486:U:C6	1:A:486:U:OP2	2.73	0.41
1:A:71:A:C6	1:A:100:G:N7	2.89	0.41
3:C:120:THR:O	3:C:124:GLU:HG3	2.21	0.41
4:D:12:ARG:HE	4:D:32:LYS:HG3	1.86	0.41
4:D:186:GLU:HB2	4:D:189:ASP:OD2	2.21	0.41
4:D:60:VAL:O	4:D:63:ILE:HG22	2.21	0.41
1:A:1073:U:OP1	5:E:61:LYS:HE2	2.21	0.41
8:H:76:ARG:HA	8:H:126:CYS:CB	2.51	0.41
9:I:6:TYR:CE2	9:I:8:THR:HG23	2.56	0.41
13:M:16:ILE:O	13:M:19:THR:OG1	2.32	0.41
13:M:2:ARG:HB3	13:M:6:ILE:HA	2.02	0.41
15:O:2:LEU:HD12	15:O:34:GLN:HE22	1.85	0.41
16:P:15:PRO:HG2	16:P:41:PRO:HG3	2.02	0.41
22:V:55:U:O4'	22:V:55:U:O2	2.39	0.41
32:8:16:ILE:HD13	32:8:25:VAL:HG22	2.02	0.40
1:A:1161:C:H5'	1:A:1162:C:OP2	2.21	0.40
1:A:675:A:H1'	11:K:117:HIS:ND1	2.37	0.40
4:D:44:LYS:HA	4:D:45:PRO:HD2	1.77	0.40
9:I:112:ARG:CG	9:I:113:LYS:N	2.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:93:LEU:O	9:I:97:LEU:HG	2.21	0.40
10:J:76:ILE:O	10:J:76:ILE:HG13	2.22	0.40
11:K:64:VAL:O	11:K:67:GLU:HB3	2.21	0.40
1:A:1156:G:O2'	1:A:1179:A:N6	2.54	0.40
1:A:147:G:H2'	1:A:148:G:H8	1.81	0.40
1:A:437:U:H3	1:A:495:A:H62	1.69	0.40
1:A:853:C:H2'	1:A:854:U:O4'	2.22	0.40
2:B:68:PHE:HD2	2:B:83:ALA:HB2	1.85	0.40
4:D:143:SER:OG	4:D:178:GLU:HA	2.22	0.40
12:L:53:ARG:NH2	12:L:61:GLU:HG2	2.29	0.40
22:V:11:C:C2	22:V:12:U:C5	3.09	0.40
22:V:58:A:HO2'	22:V:61:C:N4	2.19	0.40
1:A:155:A:H61	1:A:166:U:H3	1.69	0.40
1:A:243:A:H4'	1:A:244:U:O5'	2.21	0.40
1:A:379:C:H2'	1:A:380:G:C8	2.56	0.40
1:A:399:G:C6	1:A:400:C:C4	3.09	0.40
1:A:457:G:OP2	1:A:457:G:H8	2.04	0.40
1:A:501:C:O2	1:A:549:C:O2'	2.37	0.40
1:A:55:A:N3	1:A:55:A:H2'	2.35	0.40
1:A:942:G:C6	9:I:125:GLN:NE2	2.90	0.40
2:B:163:ILE:HD12	2:B:213:LEU:HD13	2.03	0.40
1:A:620:C:O2	4:D:131:ILE:HG12	2.21	0.40
8:H:10:LEU:HD12	8:H:76:ARG:HB2	2.03	0.40
11:K:116:PRO:HD2	21:U:27:VAL:CG2	2.36	0.40
13:M:53:ASP:HA	13:M:56:ARG:HG2	2.04	0.40
1:A:450:G:H22	16:P:13:LYS:HZ2	1.50	0.40
16:P:46:LYS:HZ3	16:P:48:GLU:HB3	1.86	0.40
23:W:46:G:C2'	23:W:46:G:N3	2.84	0.40
23:W:74:C:C2'	23:W:74:C:O2	2.68	0.40
1:A:273:U:H2'	1:A:274:A:H5'	2.03	0.40
1:A:318:G:H1	1:A:335:C:H42	1.69	0.40
1:A:402:G:H2'	1:A:403:C:H6	1.86	0.40
1:A:499:A:C6	1:A:547:A:C8	3.09	0.40
1:A:696:A:H2'	1:A:697:U:C6	2.56	0.40
3:C:141:MET:HG3	3:C:169:GLU:CD	2.42	0.40
8:H:76:ARG:HA	8:H:126:CYS:HB2	2.04	0.40
1:A:1350:A:P	9:I:119:LYS:NZ	2.91	0.40
14:N:15:LEU:HD23	14:N:18:LYS:HD2	2.02	0.40
16:P:56:ARG:HD2	16:P:56:ARG:HA	1.82	0.40
22:V:28:G:C2	22:V:29:G:C8	3.09	0.40
1:A:1015:G:C6	1:A:1016:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1256:A:H1'	1:A:1278:G:N2	2.37	0.40
1:A:1269:A:H5''	1:A:1270:G:OP2	2.22	0.40
1:A:182:A:N6	1:A:194:C:O2	2.54	0.40
1:A:247:G:C6	1:A:248:C:C4	3.09	0.40
1:A:61:G:H4'	1:A:386:C:O2'	2.21	0.40
1:A:694:A:OP1	11:K:54:SER:OG	2.36	0.40
1:A:798:U:C4	1:A:799:G:N7	2.90	0.40
1:A:91:U:H2'	1:A:92:U:C6	2.56	0.40
4:D:144:ILE:HG13	4:D:177:MET:SD	2.61	0.40
7:G:112:ASP:O	7:G:113:LYS:HB2	2.22	0.40
16:P:10:GLY:HA3	16:P:15:PRO:CA	2.49	0.40
16:P:56:ARG:NH1	16:P:59:HIS:CD2	2.90	0.40
22:V:29:G:N1	22:V:30:G:C5	2.90	0.40
22:V:62:C:O2	22:V:62:C:H2'	2.21	0.40
22:V:66:U:C2	22:V:67:C:C5	3.09	0.40
22:V:69:G:C2	22:V:70:G:C8	3.10	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/241 (90%)	188 (87%)	19 (9%)	9 (4%)	3	25
3	C	204/233 (88%)	171 (84%)	23 (11%)	10 (5%)	3	20
4	D	203/206 (98%)	190 (94%)	9 (4%)	4 (2%)	9	43
5	E	148/167 (89%)	131 (88%)	7 (5%)	10 (7%)	1	12
6	F	98/131 (75%)	81 (83%)	14 (14%)	3 (3%)	5	33
7	G	148/156 (95%)	135 (91%)	8 (5%)	5 (3%)	5	30
8	H	127/130 (98%)	110 (87%)	15 (12%)	2 (2%)	12	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/130 (96%)	106 (85%)	16 (13%)	3 (2%)	7	38
10	J	96/103 (93%)	84 (88%)	7 (7%)	5 (5%)	2	19
11	K	115/129 (89%)	104 (90%)	10 (9%)	1 (1%)	21	61
12	L	121/124 (98%)	94 (78%)	22 (18%)	5 (4%)	3	25
13	M	111/118 (94%)	99 (89%)	5 (4%)	7 (6%)	2	14
14	N	92/101 (91%)	80 (87%)	8 (9%)	4 (4%)	3	24
15	O	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	16	54
16	P	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	3
17	Q	78/84 (93%)	66 (85%)	11 (14%)	1 (1%)	15	53
18	R	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
19	S	77/92 (84%)	69 (90%)	5 (6%)	3 (4%)	4	26
20	T	83/87 (95%)	77 (93%)	5 (6%)	1 (1%)	16	54
21	U	49/71 (69%)	40 (82%)	5 (10%)	4 (8%)	1	8
25	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
26	1	60/63 (95%)	53 (88%)	5 (8%)	2 (3%)	5	31
27	2	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	11	46
28	3	54/57 (95%)	49 (91%)	3 (6%)	2 (4%)	4	28
29	4	48/55 (87%)	39 (81%)	9 (19%)	0	100	100
30	6	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	3	22
31	7	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
32	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
35	c	269/273 (98%)	251 (93%)	17 (6%)	1 (0%)	39	76
36	i	132/142 (93%)	83 (63%)	38 (29%)	11 (8%)	1	8
37	d	207/209 (99%)	194 (94%)	11 (5%)	2 (1%)	19	59
38	e	199/201 (99%)	186 (94%)	7 (4%)	6 (3%)	5	34
39	f	175/179 (98%)	157 (90%)	12 (7%)	6 (3%)	5	30
40	g	174/177 (98%)	139 (80%)	31 (18%)	4 (2%)	8	40
41	h	147/149 (99%)	122 (83%)	20 (14%)	5 (3%)	5	30
42	j	140/142 (99%)	128 (91%)	10 (7%)	2 (1%)	14	50
43	k	120/123 (98%)	112 (93%)	6 (5%)	2 (2%)	11	47
44	l	142/144 (99%)	126 (89%)	10 (7%)	6 (4%)	3	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	m	131/136 (96%)	123 (94%)	7 (5%)	1 (1%)	24	63
46	n	118/127 (93%)	111 (94%)	4 (3%)	3 (2%)	7	38
47	o	114/117 (97%)	104 (91%)	5 (4%)	5 (4%)	3	23
48	p	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	21	61
49	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
50	r	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	5	34
51	s	108/110 (98%)	103 (95%)	2 (2%)	3 (3%)	6	35
52	t	91/100 (91%)	80 (88%)	8 (9%)	3 (3%)	5	31
53	u	100/104 (96%)	77 (77%)	12 (12%)	11 (11%)	0	3
54	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
55	y	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
56	z	25/27 (93%)	20 (80%)	5 (20%)	0	100	100
All	All	5630/5985 (94%)	5003 (89%)	458 (8%)	169 (3%)	9	34

All (169) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	7	ASN
5	E	99	SER
8	H	44	PHE
9	I	57	VAL
12	L	88	ASP
16	P	11	ALA
16	P	80	LYS
19	S	4	LEU
20	T	67	HIS
21	U	26	GLY
21	U	27	VAL
21	U	30	GLU
26	1	3	ALA
28	3	56	ALA
30	6	44	VAL
36	i	65	SER
36	i	92	PRO
37	d	152	PRO
38	e	153	LEU
39	f	62	GLY
39	f	123	ASP

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Mol	Chain	Res	Type
40	g	119	ALA
41	h	41	LYS
41	h	66	ASN
41	h	67	ALA
42	j	81	ILE
44	l	29	LYS
44	l	68	SER
44	l	111	ILE
44	l	115	GLU
46	n	70	THR
46	n	119	SER
48	p	114	LEU
50	r	7	SER
51	s	65	ASP
52	t	17	SER
53	u	7	ARG
53	u	17	LYS
53	u	72	ILE
53	u	73	PHE
53	u	75	ALA
2	B	22	TRP
2	B	83	ALA
3	C	49	ALA
3	C	154	GLY
5	E	44	ARG
5	E	45	VAL
5	E	73	VAL
6	F	48	ALA
6	F	94	HIS
7	G	148	LYS
9	I	119	LYS
10	J	57	VAL
10	J	58	ASN
10	J	67	ILE
12	L	23	LEU
13	M	3	ILE
13	M	46	GLU
13	M	104	ASN
14	N	50	LEU
15	O	21	THR
16	P	10	GLY
16	P	16	PHE

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Mol	Chain	Res	Type
16	P	36	VAL
17	Q	71	SER
19	S	5	LYS
28	3	55	ILE
36	i	30	GLN
36	i	105	LEU
40	g	92	VAL
41	h	119	ASN
43	k	35	VAL
44	l	69	ARG
47	o	59	ALA
47	o	101	GLY
51	s	62	ASP
51	s	63	GLY
52	t	38	ALA
53	u	74	ASN
53	u	76	ALA
53	u	99	ASN
2	B	21	TYR
2	B	189	ASN
2	B	204	ASP
3	C	77	GLY
3	C	111	ASP
3	C	145	ALA
4	D	4	LEU
4	D	47	LEU
4	D	108	ALA
5	E	146	MET
6	F	54	LEU
7	G	114	SER
10	J	41	PRO
12	L	46	SER
13	M	5	GLY
13	M	7	ASN
13	M	23	GLY
14	N	62	ARG
16	P	49	GLY
16	P	78	VAL
21	U	24	LYS
35	c	253	LYS
36	i	59	THR
39	f	175	PHE

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Mol	Chain	Res	Type
42	j	25	LEU
43	k	108	ARG
44	l	86	GLU
45	m	69	PRO
47	o	34	HIS
47	o	66	GLY
53	u	4	LYS
3	C	3	LYS
3	C	5	HIS
5	E	11	GLN
7	G	4	ARG
9	I	112	ARG
11	K	88	PRO
13	M	47	LEU
26	1	37	LEU
27	2	4	THR
36	i	83	ALA
36	i	89	SER
38	e	62	GLN
38	e	127	GLU
39	f	121	SER
39	f	174	ASP
46	n	118	ARG
47	o	100	HIS
53	u	98	SER
2	B	63	LYS
2	B	76	SER
2	B	126	ASP
4	D	194	ILE
5	E	147	ASN
7	G	52	ARG
7	G	113	LYS
10	J	75	ASP
12	L	116	TYR
14	N	52	ARG
14	N	61	ASN
19	S	11	ASP
36	i	20	SER
38	e	80	SER
40	g	118	PRO
41	h	56	ALA
50	r	53	PHE

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Mol	Chain	Res	Type
52	t	18	GLU
2	B	30	ILE
8	H	52	GLY
30	6	45	SER
37	d	104	VAL
3	C	63	ILE
16	P	42	ILE
36	i	97	VAL
38	e	42	GLY
38	e	83	VAL
39	f	149	VAL
40	g	28	GLY
53	u	55	PRO
5	E	105	ILE
12	L	117	GLY
5	E	50	GLY
36	i	23	VAL
3	C	107	LYS
5	E	142	GLY
16	P	15	PRO
36	i	31	GLY
50	r	9	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/199 (90%)	180 (100%)	0	100	100
3	C	170/190 (90%)	170 (100%)	0	100	100
4	D	172/173 (99%)	172 (100%)	0	100	100
5	E	113/126 (90%)	113 (100%)	0	100	100
6	F	87/112 (78%)	87 (100%)	0	100	100
7	G	123/129 (95%)	123 (100%)	0	100	100
8	H	104/105 (99%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	105/107 (98%)	105 (100%)	0	100	100
10	J	86/90 (96%)	86 (100%)	0	100	100
11	K	90/99 (91%)	90 (100%)	0	100	100
12	L	103/104 (99%)	103 (100%)	0	100	100
13	M	91/96 (95%)	91 (100%)	0	100	100
14	N	79/84 (94%)	79 (100%)	0	100	100
15	O	76/77 (99%)	76 (100%)	0	100	100
16	P	65/65 (100%)	57 (88%)	8 (12%)	6	25
17	Q	74/78 (95%)	74 (100%)	0	100	100
18	R	48/65 (74%)	48 (100%)	0	100	100
19	S	70/79 (89%)	70 (100%)	0	100	100
20	T	65/66 (98%)	65 (100%)	0	100	100
21	U	44/61 (72%)	44 (100%)	0	100	100
25	0	67/68 (98%)	63 (94%)	4 (6%)	24	62
26	1	54/55 (98%)	52 (96%)	2 (4%)	41	75
27	2	48/49 (98%)	48 (100%)	0	100	100
28	3	47/48 (98%)	45 (96%)	2 (4%)	35	72
29	4	45/49 (92%)	45 (100%)	0	100	100
30	6	38/38 (100%)	37 (97%)	1 (3%)	54	82
31	7	51/52 (98%)	49 (96%)	2 (4%)	39	74
32	8	34/34 (100%)	33 (97%)	1 (3%)	50	80
35	c	216/218 (99%)	210 (97%)	6 (3%)	51	80
36	i	104/110 (94%)	87 (84%)	17 (16%)	3	13
37	d	164/164 (100%)	161 (98%)	3 (2%)	66	86
38	e	165/165 (100%)	159 (96%)	6 (4%)	42	76
39	f	148/150 (99%)	142 (96%)	6 (4%)	37	73
40	g	137/138 (99%)	133 (97%)	4 (3%)	50	80
41	h	114/114 (100%)	114 (100%)	0	100	100
42	j	116/116 (100%)	112 (97%)	4 (3%)	44	77
43	k	103/104 (99%)	101 (98%)	2 (2%)	65	85
44	l	103/103 (100%)	99 (96%)	4 (4%)	39	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	m	108/109 (99%)	107 (99%)	1 (1%)	84	93
46	n	100/103 (97%)	98 (98%)	2 (2%)	63	85
47	o	86/87 (99%)	86 (100%)	0	100	100
48	p	99/100 (99%)	95 (96%)	4 (4%)	38	74
49	q	89/90 (99%)	85 (96%)	4 (4%)	34	71
50	r	84/84 (100%)	80 (95%)	4 (5%)	31	69
51	s	93/93 (100%)	91 (98%)	2 (2%)	60	84
52	t	80/84 (95%)	77 (96%)	3 (4%)	40	75
53	u	83/85 (98%)	79 (95%)	4 (5%)	31	69
54	w	78/78 (100%)	76 (97%)	2 (3%)	54	82
55	y	56/63 (89%)	55 (98%)	1 (2%)	66	86
56	z	23/23 (100%)	13 (56%)	10 (44%)	0	0
All	All	4678/4879 (96%)	4569 (98%)	109 (2%)	61	83

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	P	6	LEU
16	P	19	VAL
16	P	33	ILE
16	P	46	LYS
16	P	55	ASP
16	P	63	GLN
16	P	68	SER
16	P	77	GLU
25	0	11	ARG
25	0	17	ASN
25	0	48	THR
25	0	57	ARG
26	1	21	LEU
26	1	38	GLN
28	3	28	LEU
28	3	29	SER
30	6	8	SER
31	7	31	HIS
31	7	47	LYS
32	8	18	LYS
35	c	5	LYS

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Mol	Chain	Res	Type
35	c	115	GLN
35	c	130	LEU
35	c	139	SER
35	c	157	SER
35	c	267	ILE
36	i	10	LEU
36	i	11	GLN
36	i	12	VAL
36	i	23	VAL
36	i	30	GLN
36	i	37	PHE
36	i	39	LYS
36	i	49	GLU
36	i	61	TYR
36	i	71	LYS
36	i	81	LYS
36	i	86	LYS
36	i	95	ASP
36	i	107	GLU
36	i	124	MET
36	i	126	ARG
36	i	135	MET
37	d	32	ASN
37	d	51	THR
37	d	91	THR
38	e	12	LEU
38	e	78	TRP
38	e	88	ARG
38	e	93	SER
38	e	126	VAL
38	e	187	VAL
39	f	5	HIS
39	f	7	TYR
39	f	19	GLU
39	f	83	TYR
39	f	117	LEU
39	f	174	ASP
40	g	29	LYS
40	g	73	ASN
40	g	80	THR
40	g	92	VAL
42	j	30	THR

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Mol	Chain	Res	Type
42	j	131	ASN
42	j	136	GLN
42	j	142	ILE
43	k	92	GLU
43	k	105	ARG
44	l	48	ARG
44	l	91	ASP
44	l	94	THR
44	l	118	THR
45	m	100	LYS
46	n	95	THR
46	n	116	VAL
48	p	8	LEU
48	p	26	VAL
48	p	37	LYS
48	p	80	VAL
49	q	5	LYS
49	q	9	ILE
49	q	16	LYS
49	q	109	LEU
50	r	46	GLU
50	r	58	VAL
50	r	60	LYS
50	r	102	SER
51	s	19	LEU
51	s	97	LEU
52	t	5	GLU
52	t	10	VAL
52	t	39	THR
53	u	15	THR
53	u	35	ILE
53	u	37	GLU
53	u	68	SER
54	w	53	LYS
54	w	76	ASP
55	y	41	ARG
56	z	4	GLN
56	z	5	LYS
56	z	9	GLU
56	z	10	GLU
56	z	12	LEU
56	z	15	THR

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Mol	Chain	Res	Type
56	z	18	TRP
56	z	20	SER
56	z	21	GLN
56	z	26	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	92	ASN
2	B	202	ASN
3	C	24	ASN
3	C	101	ASN
4	D	84	ASN
4	D	115	GLN
4	D	119	HIS
4	D	125	ASN
4	D	130	ASN
4	D	139	ASN
4	D	151	GLN
4	D	195	ASN
5	E	11	GLN
5	E	82	HIS
5	E	88	HIS
5	E	134	ASN
6	F	11	HIS
6	F	37	HIS
6	F	68	GLN
7	G	129	ASN
7	G	141	HIS
8	H	3	GLN
8	H	15	ASN
8	H	37	ASN
9	I	3	ASN
9	I	30	ASN
11	K	23	HIS
11	K	39	ASN
12	L	4	ASN
12	L	19	ASN
12	L	45	ASN
13	M	99	GLN
14	N	34	ASN
14	N	65	GLN

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Mol	Chain	Res	Type
14	N	70	HIS
15	O	34	GLN
15	O	37	HIS
15	O	41	HIS
15	O	49	HIS
15	O	50	HIS
16	P	29	ASN
16	P	59	HIS
16	P	63	GLN
17	Q	30	HIS
17	Q	50	ASN
19	S	51	HIS
19	S	56	HIS
20	T	54	GLN
20	T	67	HIS
20	T	74	HIS
32	8	37	GLN
35	c	46	ASN
36	i	30	GLN
36	i	110	GLN
37	d	150	GLN
40	g	22	GLN
40	g	38	ASN
41	h	28	ASN
41	h	73	ASN
41	h	119	ASN
41	h	128	HIS
43	k	3	GLN
51	s	61	ASN
53	u	74	ASN
55	y	57	HIS
56	z	4	GLN
56	z	21	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1530/1542 (99%)	422 (27%)	30 (1%)
22	V	75/76 (98%)	45 (60%)	9 (12%)
23	W	75/75 (100%)	40 (53%)	10 (13%)
24	X	11/11 (100%)	8 (72%)	3 (27%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	a	116/120 (96%)	43 (37%)	0
34	b	2902/2904 (99%)	1204 (41%)	0
All	All	4709/4728 (99%)	1762 (37%)	52 (1%)

All (1762) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	22	G
1	A	39	G
1	A	44	A
1	A	46	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	52	C
1	A	54	C
1	A	62	U
1	A	64	G
1	A	65	A
1	A	66	A
1	A	71	A
1	A	75	G
1	A	78	A
1	A	80	A
1	A	83	C
1	A	84	U
1	A	86	G
1	A	87	C
1	A	89	U
1	A	93	U
1	A	94	G
1	A	95	C
1	A	97	G
1	A	98	A
1	A	99	C
1	A	100	G
1	A	102	G

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Mol	Chain	Res	Type
1	A	108	G
1	A	110	C
1	A	111	G
1	A	116	A
1	A	120	A
1	A	121	U
1	A	122	G
1	A	125	U
1	A	126	G
1	A	129	A
1	A	130	A
1	A	131	A
1	A	133	U
1	A	141	G
1	A	144	G
1	A	145	G
1	A	146	G
1	A	149	A
1	A	152	A
1	A	157	U
1	A	160	A
1	A	163	C
1	A	179	A
1	A	182	A
1	A	183	C
1	A	184	G
1	A	185	U
1	A	186	C
1	A	187	G
1	A	188	C
1	A	192	A
1	A	196	A
1	A	197	A
1	A	198	G
1	A	200	G
1	A	201	G
1	A	203	G
1	A	204	G
1	A	205	A
1	A	210	C
1	A	211	G
1	A	215	C

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Mol	Chain	Res	Type
1	A	217	C
1	A	218	U
1	A	219	U
1	A	226	G
1	A	229	U
1	A	230	G
1	A	231	U
1	A	236	A
1	A	238	A
1	A	239	U
1	A	240	G
1	A	244	U
1	A	245	U
1	A	247	G
1	A	251	G
1	A	255	G
1	A	256	U
1	A	257	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	275	G
1	A	277	C
1	A	280	C
1	A	281	G
1	A	289	G
1	A	302	G
1	A	309	A
1	A	314	C
1	A	320	A
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	342	C
1	A	343	U
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	368	U

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Mol	Chain	Res	Type
1	A	369	G
1	A	372	C
1	A	373	A
1	A	374	A
1	A	375	U
1	A	377	G
1	A	381	C
1	A	386	C
1	A	387	U
1	A	388	G
1	A	389	A
1	A	390	U
1	A	391	G
1	A	397	A
1	A	398	U
1	A	399	G
1	A	401	C
1	A	404	G
1	A	406	G
1	A	408	A
1	A	411	A
1	A	413	G
1	A	414	A
1	A	416	G
1	A	429	U
1	A	430	A
1	A	435	A
1	A	437	U
1	A	439	U
1	A	448	A
1	A	451	A
1	A	452	A
1	A	455	G
1	A	456	A
1	A	457	G
1	A	461	A
1	A	462	G
1	A	463	U
1	A	464	U
1	A	466	A
1	A	468	A
1	A	469	C

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Mol	Chain	Res	Type
1	A	475	C
1	A	476	U
1	A	479	U
1	A	481	G
1	A	483	C
1	A	484	G
1	A	485	U
1	A	486	U
1	A	492	C
1	A	497	G
1	A	499	A
1	A	501	C
1	A	511	C
1	A	517	G
1	A	518	C
1	A	527	G
1	A	532	A
1	A	533	A
1	A	540	G
1	A	541	G
1	A	542	G
1	A	543	U
1	A	547	A
1	A	548	G
1	A	549	C
1	A	557	G
1	A	563	A
1	A	564	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	579	A
1	A	588	G
1	A	589	U
1	A	591	U
1	A	592	G
1	A	593	U
1	A	598	U
1	A	607	A
1	A	608	A

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Mol	Chain	Res	Type
1	A	614	C
1	A	615	G
1	A	618	C
1	A	619	U
1	A	621	A
1	A	632	U
1	A	633	G
1	A	636	U
1	A	637	C
1	A	638	U
1	A	639	G
1	A	648	A
1	A	653	U
1	A	654	G
1	A	665	A
1	A	683	G
1	A	687	A
1	A	696	A
1	A	697	U
1	A	698	G
1	A	699	C
1	A	700	G
1	A	701	U
1	A	702	A
1	A	703	G
1	A	711	G
1	A	718	A
1	A	719	C
1	A	721	G
1	A	723	U
1	A	724	G
1	A	729	A
1	A	731	G
1	A	747	A
1	A	753	A
1	A	755	G
1	A	763	G
1	A	765	G
1	A	766	A
1	A	780	A
1	A	785	G
1	A	792	A

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Mol	Chain	Res	Type
1	A	793	U
1	A	794	A
1	A	795	C
1	A	809	G
1	A	810	C
1	A	815	A
1	A	817	C
1	A	819	A
1	A	823	C
1	A	828	U
1	A	832	G
1	A	840	C
1	A	841	C
1	A	842	U
1	A	843	U
1	A	846	G
1	A	849	G
1	A	851	G
1	A	854	U
1	A	868	C
1	A	873	A
1	A	884	U
1	A	885	G
1	A	891	U
1	A	900	A
1	A	914	A
1	A	915	A
1	A	918	A
1	A	927	G
1	A	934	C
1	A	935	A
1	A	936	C
1	A	939	G
1	A	955	U
1	A	960	U
1	A	961	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A

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Mol	Chain	Res	Type
1	A	976	G
1	A	977	A
1	A	985	C
1	A	989	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	996	A
1	A	1004	A
1	A	1006	G
1	A	1010	U
1	A	1013	G
1	A	1020	G
1	A	1022	A
1	A	1025	U
1	A	1026	G
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1032	G
1	A	1036	A
1	A	1051	C
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1070	U
1	A	1073	U
1	A	1086	U
1	A	1093	A
1	A	1094	G
1	A	1095	U
1	A	1100	C
1	A	1101	A
1	A	1108	G
1	A	1112	C
1	A	1118	U
1	A	1121	U
1	A	1130	A
1	A	1135	U
1	A	1136	C
1	A	1137	C
1	A	1139	G

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Mol	Chain	Res	Type
1	A	1140	C
1	A	1143	G
1	A	1158	C
1	A	1159	U
1	A	1161	C
1	A	1167	A
1	A	1168	U
1	A	1184	G
1	A	1192	C
1	A	1196	A
1	A	1197	A
1	A	1198	G
1	A	1199	U
1	A	1202	U
1	A	1209	C
1	A	1210	C
1	A	1215	G
1	A	1218	C
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1249	C
1	A	1251	A
1	A	1253	G
1	A	1256	A
1	A	1258	G
1	A	1274	A
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1281	C
1	A	1282	C
1	A	1287	A
1	A	1290	G
1	A	1295	U
1	A	1300	G
1	A	1301	U
1	A	1302	C

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Mol	Chain	Res	Type
1	A	1303	C
1	A	1305	G
1	A	1312	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1323	G
1	A	1333	A
1	A	1335	U
1	A	1336	C
1	A	1338	G
1	A	1341	U
1	A	1342	C
1	A	1343	G
1	A	1345	U
1	A	1346	A
1	A	1349	A
1	A	1353	G
1	A	1357	A
1	A	1361	G
1	A	1362	A
1	A	1363	A
1	A	1364	U
1	A	1368	A
1	A	1379	G
1	A	1398	A
1	A	1402	C
1	A	1415	G
1	A	1419	G
1	A	1422	G
1	A	1425	U
1	A	1441	A
1	A	1446	A
1	A	1451	U
1	A	1452	C
1	A	1470	U
1	A	1490	U
1	A	1493	A
1	A	1494	G
1	A	1496	C
1	A	1497	G

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Mol	Chain	Res	Type
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1518	A
1	A	1520	C
1	A	1523	G
1	A	1528	U
1	A	1530	G
1	A	1534	A
22	V	2	C
22	V	3	C
22	V	4	C
22	V	5	G
22	V	6	G
22	V	8	U
22	V	15	G
22	V	16	U
22	V	17	C
22	V	18	G
22	V	19	G
22	V	20	U
22	V	21	A
22	V	22	G
22	V	26	A
22	V	28	G
22	V	37	A
22	V	38	A
22	V	39	U
22	V	40	C
22	V	41	C
22	V	42	C
22	V	43	C
22	V	44	G
22	V	46	G
22	V	47	U
22	V	48	C
22	V	51	U
22	V	53	G
22	V	54	U
22	V	55	U
22	V	57	G
22	V	59	U

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Mol	Chain	Res	Type
22	V	60	U
22	V	62	C
22	V	64	A
22	V	65	G
22	V	66	U
22	V	68	C
22	V	71	G
22	V	72	C
22	V	73	A
22	V	74	C
22	V	75	C
22	V	76	A
23	W	2	G
23	W	6	C
23	W	8	U
23	W	13	C
23	W	15	G
23	W	16	C
23	W	17	U
23	W	18	G
23	W	19	G
23	W	20	U
23	W	21	A
23	W	22	G
23	W	28	C
23	W	34	G
23	W	35	C
23	W	37	G
23	W	40	U
23	W	42	G
23	W	43	G
23	W	46	G
23	W	48	C
23	W	49	G
23	W	50	G
23	W	52	G
23	W	55	U
23	W	56	C
23	W	57	A
23	W	58	A
23	W	59	A
23	W	60	U

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Mol	Chain	Res	Type
23	W	61	C
23	W	62	C
23	W	66	C
23	W	67	G
23	W	69	G
23	W	71	C
23	W	72	G
23	W	73	A
23	W	74	C
23	W	75	A
24	X	13	U
24	X	14	G
24	X	16	C
24	X	17	C
24	X	18	C
24	X	19	U
24	X	20	C
24	X	21	A
33	a	4	C
33	a	7	G
33	a	9	G
33	a	10	G
33	a	12	C
33	a	13	G
33	a	15	A
33	a	21	G
33	a	24	G
33	a	26	C
33	a	30	C
33	a	34	A
33	a	35	C
33	a	42	C
33	a	43	C
33	a	44	G
33	a	46	A
33	a	52	A
33	a	53	A
33	a	54	G
33	a	56	G
33	a	57	A
33	a	59	A
33	a	65	U

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Mol	Chain	Res	Type
33	a	67	G
33	a	84	G
33	a	85	G
33	a	86	G
33	a	87	U
33	a	88	C
33	a	89	U
33	a	90	C
33	a	91	C
33	a	93	C
33	a	98	G
33	a	99	A
33	a	100	G
33	a	103	U
33	a	106	G
33	a	108	A
33	a	109	A
33	a	110	C
33	a	115	A
34	b	3	U
34	b	4	U
34	b	7	G
34	b	10	A
34	b	12	U
34	b	13	A
34	b	14	A
34	b	20	C
34	b	23	G
34	b	24	G
34	b	28	A
34	b	33	C
34	b	34	U
34	b	35	G
34	b	39	G
34	b	45	G
34	b	46	G
34	b	49	A
34	b	50	U
34	b	51	G
34	b	55	G
34	b	62	U
34	b	63	A

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Mol	Chain	Res	Type
34	b	64	A
34	b	69	C
34	b	71	A
34	b	72	U
34	b	73	A
34	b	74	A
34	b	75	G
34	b	76	C
34	b	77	G
34	b	84	A
34	b	86	G
34	b	88	G
34	b	90	U
34	b	91	A
34	b	92	U
34	b	96	C
34	b	100	U
34	b	101	A
34	b	102	U
34	b	103	A
34	b	109	C
34	b	114	U
34	b	116	C
34	b	118	A
34	b	119	A
34	b	120	U
34	b	125	A
34	b	126	A
34	b	127	A
34	b	136	G
34	b	140	C
34	b	142	A
34	b	160	A
34	b	163	C
34	b	166	U
34	b	169	G
34	b	172	A
34	b	174	U
34	b	181	A
34	b	186	G
34	b	187	G
34	b	188	G

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Mol	Chain	Res	Type
34	b	195	A
34	b	196	A
34	b	197	A
34	b	199	A
34	b	200	U
34	b	201	C
34	b	204	A
34	b	210	C
34	b	215	G
34	b	216	A
34	b	218	A
34	b	221	A
34	b	222	A
34	b	223	A
34	b	224	U
34	b	225	C
34	b	228	C
34	b	229	C
34	b	231	A
34	b	233	A
34	b	234	U
34	b	235	U
34	b	239	C
34	b	240	C
34	b	241	A
34	b	242	G
34	b	243	U
34	b	245	G
34	b	248	G
34	b	249	C
34	b	250	G
34	b	251	A
34	b	252	G
34	b	255	A
34	b	256	A
34	b	264	C
34	b	265	A
34	b	266	G
34	b	268	C
34	b	270	A
34	b	271	G
34	b	272	A

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Mol	Chain	Res	Type
34	b	274	C
34	b	275	C
34	b	277	G
34	b	278	A
34	b	279	A
34	b	280	U
34	b	281	C
34	b	282	A
34	b	288	U
34	b	290	U
34	b	294	A
34	b	295	G
34	b	298	G
34	b	299	A
34	b	300	A
34	b	303	G
34	b	304	U
34	b	307	G
34	b	309	A
34	b	310	A
34	b	311	A
34	b	317	G
34	b	322	A
34	b	323	C
34	b	324	A
34	b	329	G
34	b	330	A
34	b	331	C
34	b	332	A
34	b	342	A
34	b	343	C
34	b	345	A
34	b	347	A
34	b	349	U
34	b	353	C
34	b	356	G
34	b	358	U
34	b	362	A
34	b	363	G
34	b	365	U
34	b	366	C
34	b	367	G

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Mol	Chain	Res	Type
34	b	368	A
34	b	369	U
34	b	370	G
34	b	371	A
34	b	372	G
34	b	373	U
34	b	375	G
34	b	383	C
34	b	385	C
34	b	386	G
34	b	387	U
34	b	388	G
34	b	389	G
34	b	391	A
34	b	396	G
34	b	400	G
34	b	401	A
34	b	403	U
34	b	404	A
34	b	405	U
34	b	406	G
34	b	411	G
34	b	412	A
34	b	413	C
34	b	419	U
34	b	425	G
34	b	434	U
34	b	436	C
34	b	442	G
34	b	443	A
34	b	444	C
34	b	446	G
34	b	447	A
34	b	448	U
34	b	449	A
34	b	451	U
34	b	453	A
34	b	454	A
34	b	456	C
34	b	457	A
34	b	459	U
34	b	461	C

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Mol	Chain	Res	Type
34	b	464	U
34	b	466	A
34	b	478	A
34	b	479	A
34	b	480	A
34	b	481	G
34	b	482	A
34	b	483	A
34	b	489	G
34	b	490	C
34	b	491	G
34	b	493	G
34	b	494	G
34	b	501	A
34	b	502	A
34	b	503	A
34	b	504	A
34	b	505	A
34	b	507	A
34	b	508	A
34	b	509	C
34	b	513	A
34	b	517	C
34	b	518	G
34	b	519	U
34	b	521	U
34	b	527	C
34	b	528	A
34	b	529	A
34	b	530	G
34	b	531	C
34	b	532	A
34	b	538	A
34	b	539	G
34	b	544	C
34	b	545	U
34	b	546	U
34	b	547	A
34	b	548	G
34	b	549	G
34	b	550	C
34	b	551	G

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Mol	Chain	Res	Type
34	b	556	A
34	b	560	C
34	b	563	A
34	b	567	U
34	b	568	U
34	b	569	U
34	b	573	U
34	b	574	A
34	b	575	A
34	b	578	G
34	b	584	C
34	b	585	G
34	b	586	A
34	b	587	C
34	b	589	U
34	b	591	U
34	b	592	A
34	b	603	A
34	b	604	G
34	b	605	G
34	b	606	U
34	b	612	G
34	b	613	A
34	b	614	A
34	b	619	G
34	b	621	A
34	b	622	G
34	b	625	G
34	b	626	A
34	b	627	A
34	b	633	A
34	b	637	A
34	b	638	G
34	b	640	C
34	b	643	A
34	b	644	A
34	b	646	U
34	b	647	G
34	b	651	G
34	b	652	U
34	b	653	U
34	b	654	A

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Mol	Chain	Res	Type
34	b	655	A
34	b	656	G
34	b	659	G
34	b	664	G
34	b	665	U
34	b	667	U
34	b	668	A
34	b	669	G
34	b	670	A
34	b	675	A
34	b	679	C
34	b	683	U
34	b	686	U
34	b	687	C
34	b	695	G
34	b	701	G
34	b	704	G
34	b	705	A
34	b	711	G
34	b	715	A
34	b	716	A
34	b	718	A
34	b	719	C
34	b	723	C
34	b	724	U
34	b	727	A
34	b	729	G
34	b	730	A
34	b	731	C
34	b	733	G
34	b	738	G
34	b	740	C
34	b	745	G
34	b	747	U
34	b	750	A
34	b	752	A
34	b	757	G
34	b	758	C
34	b	764	A
34	b	765	C
34	b	766	U
34	b	770	G

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Mol	Chain	Res	Type
34	b	775	G
34	b	776	G
34	b	777	G
34	b	781	A
34	b	782	A
34	b	783	A
34	b	784	G
34	b	785	G
34	b	788	A
34	b	789	A
34	b	790	U
34	b	792	A
34	b	793	A
34	b	794	A
34	b	797	G
34	b	801	G
34	b	805	G
34	b	807	U
34	b	810	U
34	b	812	C
34	b	814	C
34	b	819	A
34	b	822	G
34	b	827	U
34	b	828	U
34	b	829	A
34	b	830	G
34	b	836	G
34	b	842	U
34	b	844	A
34	b	845	A
34	b	846	U
34	b	847	U
34	b	852	U
34	b	856	G
34	b	858	G
34	b	859	G
34	b	866	A
34	b	867	C
34	b	872	U
34	b	873	C
34	b	874	G

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Mol	Chain	Res	Type
34	b	876	C
34	b	877	A
34	b	878	A
34	b	879	G
34	b	880	G
34	b	881	G
34	b	882	G
34	b	886	A
34	b	887	U
34	b	888	C
34	b	889	C
34	b	891	G
34	b	893	C
34	b	894	U
34	b	895	U
34	b	896	A
34	b	897	C
34	b	898	C
34	b	899	A
34	b	900	A
34	b	910	A
34	b	911	A
34	b	912	C
34	b	914	G
34	b	915	C
34	b	929	U
34	b	931	U
34	b	932	U
34	b	933	A
34	b	934	U
34	b	941	A
34	b	945	A
34	b	946	C
34	b	947	A
34	b	954	G
34	b	958	U
34	b	959	A
34	b	961	C
34	b	967	U
34	b	969	G
34	b	973	A
34	b	974	G

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Mol	Chain	Res	Type
34	b	975	A
34	b	979	A
34	b	980	A
34	b	983	A
34	b	985	C
34	b	986	C
34	b	988	A
34	b	990	A
34	b	996	A
34	b	999	U
34	b	1003	G
34	b	1004	U
34	b	1006	C
34	b	1007	C
34	b	1008	A
34	b	1010	A
34	b	1011	G
34	b	1012	U
34	b	1013	C
34	b	1017	G
34	b	1018	U
34	b	1021	A
34	b	1022	G
34	b	1023	U
34	b	1025	G
34	b	1026	G
34	b	1027	A
34	b	1028	A
34	b	1032	A
34	b	1033	U
34	b	1034	G
34	b	1037	G
34	b	1038	G
34	b	1039	A
34	b	1045	C
34	b	1047	G
34	b	1051	G
34	b	1052	C
34	b	1054	A
34	b	1055	G
34	b	1056	G
34	b	1057	A

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Mol	Chain	Res	Type
34	b	1058	U
34	b	1059	G
34	b	1060	U
34	b	1061	U
34	b	1062	G
34	b	1063	G
34	b	1064	C
34	b	1068	G
34	b	1069	A
34	b	1070	A
34	b	1071	G
34	b	1072	C
34	b	1073	A
34	b	1075	C
34	b	1077	A
34	b	1078	U
34	b	1079	C
34	b	1080	A
34	b	1081	U
34	b	1082	U
34	b	1084	A
34	b	1085	A
34	b	1086	A
34	b	1087	G
34	b	1088	A
34	b	1089	A
34	b	1090	A
34	b	1091	G
34	b	1092	C
34	b	1094	U
34	b	1095	A
34	b	1096	A
34	b	1097	U
34	b	1098	A
34	b	1099	G
34	b	1100	C
34	b	1102	C
34	b	1103	A
34	b	1104	C
34	b	1105	U
34	b	1106	G
34	b	1107	G

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Mol	Chain	Res	Type
34	b	1109	C
34	b	1110	G
34	b	1111	A
34	b	1112	G
34	b	1115	G
34	b	1116	G
34	b	1117	C
34	b	1121	C
34	b	1122	G
34	b	1130	U
34	b	1132	U
34	b	1133	A
34	b	1134	A
34	b	1135	C
34	b	1136	G
34	b	1141	U
34	b	1142	A
34	b	1143	A
34	b	1144	A
34	b	1151	A
34	b	1155	A
34	b	1156	A
34	b	1163	G
34	b	1169	A
34	b	1171	G
34	b	1172	C
34	b	1173	U
34	b	1174	U
34	b	1175	A
34	b	1176	U
34	b	1177	G
34	b	1178	C
34	b	1179	G
34	b	1180	U
34	b	1184	U
34	b	1185	G
34	b	1187	G
34	b	1188	U
34	b	1195	G
34	b	1197	G
34	b	1200	C
34	b	1202	G

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Mol	Chain	Res	Type
34	b	1204	A
34	b	1205	A
34	b	1206	G
34	b	1209	U
34	b	1210	G
34	b	1211	C
34	b	1212	G
34	b	1218	G
34	b	1222	U
34	b	1223	G
34	b	1224	U
34	b	1225	G
34	b	1227	G
34	b	1232	G
34	b	1236	G
34	b	1237	A
34	b	1238	G
34	b	1239	G
34	b	1240	U
34	b	1241	A
34	b	1242	U
34	b	1244	A
34	b	1247	A
34	b	1248	G
34	b	1249	U
34	b	1252	G
34	b	1253	A
34	b	1255	U
34	b	1256	G
34	b	1260	A
34	b	1265	A
34	b	1266	G
34	b	1268	A
34	b	1271	G
34	b	1272	A
34	b	1273	U
34	b	1274	A
34	b	1276	A
34	b	1280	G
34	b	1287	A
34	b	1294	U
34	b	1296	G

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Mol	Chain	Res	Type
34	b	1299	G
34	b	1300	G
34	b	1301	A
34	b	1302	A
34	b	1306	C
34	b	1312	U
34	b	1314	C
34	b	1318	U
34	b	1320	C
34	b	1321	A
34	b	1322	A
34	b	1330	C
34	b	1332	G
34	b	1338	G
34	b	1340	U
34	b	1341	G
34	b	1345	C
34	b	1347	A
34	b	1348	C
34	b	1349	C
34	b	1352	U
34	b	1354	A
34	b	1355	G
34	b	1365	A
34	b	1368	G
34	b	1370	C
34	b	1374	G
34	b	1378	A
34	b	1379	U
34	b	1381	G
34	b	1382	G
34	b	1383	A
34	b	1386	C
34	b	1390	U
34	b	1392	A
34	b	1394	U
34	b	1395	A
34	b	1396	U
34	b	1400	U
34	b	1414	C
34	b	1415	U
34	b	1416	G

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Mol	Chain	Res	Type
34	b	1418	G
34	b	1419	A
34	b	1420	A
34	b	1421	G
34	b	1424	G
34	b	1425	G
34	b	1427	A
34	b	1428	C
34	b	1444	G
34	b	1449	G
34	b	1451	C
34	b	1452	G
34	b	1453	A
34	b	1454	C
34	b	1455	G
34	b	1458	U
34	b	1459	G
34	b	1460	U
34	b	1461	C
34	b	1467	U
34	b	1469	A
34	b	1470	A
34	b	1476	U
34	b	1477	A
34	b	1478	G
34	b	1482	G
34	b	1485	U
34	b	1488	C
34	b	1490	A
34	b	1491	G
34	b	1493	C
34	b	1494	A
34	b	1496	A
34	b	1497	U
34	b	1498	C
34	b	1501	G
34	b	1503	A
34	b	1504	A
34	b	1506	U
34	b	1507	C
34	b	1508	A
34	b	1509	A

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Mol	Chain	Res	Type
34	b	1510	G
34	b	1511	G
34	b	1512	C
34	b	1521	G
34	b	1522	A
34	b	1523	U
34	b	1524	G
34	b	1529	G
34	b	1530	G
34	b	1535	A
34	b	1536	C
34	b	1537	G
34	b	1539	U
34	b	1542	U
34	b	1550	C
34	b	1552	A
34	b	1556	C
34	b	1562	U
34	b	1565	C
34	b	1566	A
34	b	1568	G
34	b	1569	A
34	b	1570	A
34	b	1576	U
34	b	1578	U
34	b	1583	A
34	b	1585	C
34	b	1587	G
34	b	1600	C
34	b	1602	U
34	b	1603	A
34	b	1607	C
34	b	1608	A
34	b	1609	A
34	b	1610	A
34	b	1613	G
34	b	1614	A
34	b	1616	A
34	b	1617	C
34	b	1618	A
34	b	1627	G
34	b	1631	G

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Mol	Chain	Res	Type
34	b	1633	G
34	b	1634	A
34	b	1637	A
34	b	1644	C
34	b	1646	C
34	b	1647	U
34	b	1648	U
34	b	1649	G
34	b	1654	A
34	b	1656	C
34	b	1657	U
34	b	1658	C
34	b	1660	G
34	b	1663	G
34	b	1667	G
34	b	1668	A
34	b	1670	C
34	b	1672	A
34	b	1673	G
34	b	1674	G
34	b	1677	A
34	b	1689	A
34	b	1691	C
34	b	1693	U
34	b	1694	C
34	b	1698	A
34	b	1699	G
34	b	1700	A
34	b	1702	G
34	b	1703	G
34	b	1705	A
34	b	1706	C
34	b	1710	G
34	b	1713	A
34	b	1715	G
34	b	1716	U
34	b	1728	C
34	b	1730	C
34	b	1731	G
34	b	1732	C
34	b	1733	G
34	b	1735	A

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Mol	Chain	Res	Type
34	b	1746	A
34	b	1750	G
34	b	1754	A
34	b	1756	G
34	b	1757	A
34	b	1758	U
34	b	1763	G
34	b	1764	C
34	b	1766	G
34	b	1773	A
34	b	1774	C
34	b	1775	U
34	b	1776	G
34	b	1778	U
34	b	1780	A
34	b	1782	U
34	b	1783	A
34	b	1784	A
34	b	1786	A
34	b	1787	A
34	b	1800	C
34	b	1801	A
34	b	1802	A
34	b	1805	A
34	b	1806	C
34	b	1807	G
34	b	1808	A
34	b	1809	A
34	b	1811	G
34	b	1819	A
34	b	1820	U
34	b	1827	U
34	b	1828	G
34	b	1829	A
34	b	1833	C
34	b	1839	G
34	b	1842	G
34	b	1845	G
34	b	1847	A
34	b	1848	A
34	b	1849	G
34	b	1853	A

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Mol	Chain	Res	Type
34	b	1857	G
34	b	1862	G
34	b	1866	A
34	b	1867	G
34	b	1868	C
34	b	1870	C
34	b	1871	A
34	b	1875	G
34	b	1877	A
34	b	1885	A
34	b	1890	A
34	b	1896	G
34	b	1901	A
34	b	1902	C
34	b	1905	C
34	b	1907	G
34	b	1908	C
34	b	1911	U
34	b	1912	A
34	b	1913	A
34	b	1914	C
34	b	1915	U
34	b	1924	C
34	b	1928	A
34	b	1929	G
34	b	1930	G
34	b	1931	U
34	b	1932	A
34	b	1936	A
34	b	1937	A
34	b	1938	A
34	b	1940	U
34	b	1941	C
34	b	1942	C
34	b	1943	U
34	b	1952	A
34	b	1953	A
34	b	1955	U
34	b	1958	C
34	b	1960	A
34	b	1961	C
34	b	1963	U

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Mol	Chain	Res	Type
34	b	1964	G
34	b	1965	C
34	b	1967	C
34	b	1970	A
34	b	1971	U
34	b	1972	G
34	b	1977	A
34	b	1980	G
34	b	1981	A
34	b	1982	U
34	b	1989	G
34	b	1991	U
34	b	1993	U
34	b	1997	C
34	b	2006	C
34	b	2007	U
34	b	2011	U
34	b	2014	A
34	b	2020	A
34	b	2022	U
34	b	2023	C
34	b	2025	C
34	b	2027	G
34	b	2030	A
34	b	2031	A
34	b	2032	G
34	b	2033	A
34	b	2034	U
34	b	2036	C
34	b	2042	A
34	b	2043	C
34	b	2044	C
34	b	2046	G
34	b	2049	G
34	b	2055	C
34	b	2056	G
34	b	2060	A
34	b	2061	G
34	b	2062	A
34	b	2063	C
34	b	2068	U
34	b	2069	G

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Mol	Chain	Res	Type
34	b	2070	A
34	b	2076	U
34	b	2077	A
34	b	2080	A
34	b	2087	G
34	b	2092	U
34	b	2095	A
34	b	2098	U
34	b	2103	C
34	b	2104	C
34	b	2105	U
34	b	2106	U
34	b	2107	G
34	b	2109	U
34	b	2110	G
34	b	2111	U
34	b	2112	G
34	b	2113	U
34	b	2114	A
34	b	2115	G
34	b	2117	A
34	b	2118	U
34	b	2119	A
34	b	2120	G
34	b	2121	G
34	b	2123	G
34	b	2124	G
34	b	2125	G
34	b	2126	A
34	b	2127	G
34	b	2128	G
34	b	2130	U
34	b	2131	U
34	b	2132	U
34	b	2133	G
34	b	2139	U
34	b	2142	A
34	b	2143	C
34	b	2144	G
34	b	2145	C
34	b	2147	A
34	b	2148	G

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Mol	Chain	Res	Type
34	b	2149	U
34	b	2152	G
34	b	2153	C
34	b	2156	G
34	b	2158	A
34	b	2159	G
34	b	2160	C
34	b	2161	C
34	b	2162	G
34	b	2163	A
34	b	2164	C
34	b	2165	C
34	b	2166	U
34	b	2167	U
34	b	2168	G
34	b	2169	A
34	b	2170	A
34	b	2171	A
34	b	2172	U
34	b	2173	A
34	b	2174	C
34	b	2175	C
34	b	2176	A
34	b	2177	C
34	b	2178	C
34	b	2179	C
34	b	2183	A
34	b	2185	U
34	b	2190	G
34	b	2191	A
34	b	2193	G
34	b	2198	A
34	b	2199	A
34	b	2203	U
34	b	2204	G
34	b	2210	U
34	b	2211	A
34	b	2212	A
34	b	2213	U
34	b	2214	C
34	b	2215	C
34	b	2218	G

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Mol	Chain	Res	Type
34	b	2225	A
34	b	2238	G
34	b	2239	G
34	b	2243	U
34	b	2250	G
34	b	2251	G
34	b	2252	G
34	b	2255	G
34	b	2256	G
34	b	2257	U
34	b	2261	C
34	b	2265	U
34	b	2267	A
34	b	2268	A
34	b	2273	A
34	b	2275	C
34	b	2276	G
34	b	2279	G
34	b	2280	G
34	b	2282	G
34	b	2283	C
34	b	2284	A
34	b	2286	G
34	b	2287	A
34	b	2288	A
34	b	2289	G
34	b	2294	G
34	b	2297	A
34	b	2298	A
34	b	2305	U
34	b	2307	G
34	b	2308	G
34	b	2311	A
34	b	2312	U
34	b	2316	G
34	b	2319	G
34	b	2320	U
34	b	2322	A
34	b	2325	G
34	b	2327	A
34	b	2331	G
34	b	2333	A

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Mol	Chain	Res	Type
34	b	2334	U
34	b	2335	A
34	b	2336	A
34	b	2345	G
34	b	2347	C
34	b	2350	C
34	b	2353	G
34	b	2354	C
34	b	2357	G
34	b	2358	A
34	b	2361	G
34	b	2366	A
34	b	2367	G
34	b	2371	G
34	b	2372	U
34	b	2376	A
34	b	2379	G
34	b	2382	G
34	b	2383	G
34	b	2385	C
34	b	2388	A
34	b	2396	G
34	b	2402	U
34	b	2403	C
34	b	2404	U
34	b	2406	A
34	b	2407	A
34	b	2410	G
34	b	2411	A
34	b	2413	G
34	b	2421	G
34	b	2422	C
34	b	2423	U
34	b	2425	A
34	b	2426	A
34	b	2427	C
34	b	2428	G
34	b	2429	G
34	b	2430	A
34	b	2431	U
34	b	2434	A
34	b	2435	A

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Mol	Chain	Res	Type
34	b	2439	A
34	b	2440	C
34	b	2441	U
34	b	2445	G
34	b	2447	G
34	b	2448	A
34	b	2449	U
34	b	2450	A
34	b	2455	G
34	b	2456	C
34	b	2458	G
34	b	2459	A
34	b	2465	C
34	b	2470	G
34	b	2472	G
34	b	2474	U
34	b	2476	A
34	b	2478	A
34	b	2481	G
34	b	2482	A
34	b	2484	G
34	b	2490	G
34	b	2491	U
34	b	2497	A
34	b	2500	U
34	b	2502	G
34	b	2503	A
34	b	2505	G
34	b	2506	U
34	b	2507	C
34	b	2513	A
34	b	2517	C
34	b	2518	A
34	b	2519	U
34	b	2525	G
34	b	2527	C
34	b	2529	G
34	b	2530	A
34	b	2534	A
34	b	2535	G
34	b	2536	G
34	b	2544	G

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Mol	Chain	Res	Type
34	b	2547	A
34	b	2554	U
34	b	2556	C
34	b	2557	G
34	b	2562	U
34	b	2564	A
34	b	2565	A
34	b	2566	A
34	b	2567	G
34	b	2571	U
34	b	2573	C
34	b	2576	G
34	b	2577	A
34	b	2578	G
34	b	2582	G
34	b	2584	U
34	b	2585	U
34	b	2586	U
34	b	2590	A
34	b	2595	G
34	b	2596	U
34	b	2600	A
34	b	2601	C
34	b	2602	A
34	b	2603	G
34	b	2604	U
34	b	2607	G
34	b	2609	U
34	b	2610	C
34	b	2611	C
34	b	2613	U
34	b	2614	A
34	b	2615	U
34	b	2618	G
34	b	2623	G
34	b	2628	C
34	b	2629	U
34	b	2634	A
34	b	2635	A
34	b	2638	G
34	b	2639	A
34	b	2640	G

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Mol	Chain	Res	Type
34	b	2641	G
34	b	2645	G
34	b	2646	C
34	b	2655	G
34	b	2659	G
34	b	2660	A
34	b	2661	G
34	b	2666	C
34	b	2670	A
34	b	2673	G
34	b	2688	G
34	b	2689	U
34	b	2690	U
34	b	2692	G
34	b	2700	A
34	b	2702	G
34	b	2707	U
34	b	2712	C
34	b	2713	U
34	b	2716	C
34	b	2718	G
34	b	2726	A
34	b	2727	A
34	b	2732	G
34	b	2733	A
34	b	2735	G
34	b	2736	A
34	b	2744	G
34	b	2745	C
34	b	2746	U
34	b	2749	A
34	b	2750	A
34	b	2751	G
34	b	2752	C
34	b	2753	A
34	b	2755	C
34	b	2757	A
34	b	2758	A
34	b	2761	A
34	b	2762	C
34	b	2765	A
34	b	2767	C

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Mol	Chain	Res	Type
34	b	2772	C
34	b	2778	A
34	b	2779	U
34	b	2780	G
34	b	2781	A
34	b	2782	G
34	b	2784	U
34	b	2792	A
34	b	2793	C
34	b	2795	C
34	b	2796	U
34	b	2797	U
34	b	2798	U
34	b	2799	A
34	b	2800	A
34	b	2805	C
34	b	2808	G
34	b	2818	U
34	b	2819	G
34	b	2820	A
34	b	2821	A
34	b	2823	A
34	b	2824	C
34	b	2826	A
34	b	2833	U
34	b	2835	A
34	b	2838	G
34	b	2849	U
34	b	2850	A
34	b	2858	C
34	b	2861	U
34	b	2866	U
34	b	2868	A
34	b	2872	A
34	b	2873	A
34	b	2874	C
34	b	2883	A
34	b	2884	U
34	b	2885	G
34	b	2886	A
34	b	2888	C
34	b	2891	U

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Mol	Chain	Res	Type
34	b	2893	A
34	b	2894	G
34	b	2895	G
34	b	2901	C
34	b	2903	U

All (52) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	51	A
1	A	66	A
1	A	94	G
1	A	109	A
1	A	125	U
1	A	148	G
1	A	218	U
1	A	243	A
1	A	254	G
1	A	301	G
1	A	429	U
1	A	447	G
1	A	478	A
1	A	484	G
1	A	572	A
1	A	695	A
1	A	701	U
1	A	722	G
1	A	960	U
1	A	1065	U
1	A	1117	A
1	A	1129	C
1	A	1157	A
1	A	1201	A
1	A	1226	C
1	A	1300	G
1	A	1332	A
1	A	1348	U
1	A	1492	A
22	V	9	A
22	V	15	G
22	V	18	G

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Mol	Chain	Res	Type
22	V	38	A
22	V	39	U
22	V	40	C
22	V	48	C
22	V	74	C
22	V	75	C
23	W	1	C
23	W	7	G
23	W	18	G
23	W	20	U
23	W	42	G
23	W	49	G
23	W	57	A
23	W	60	U
23	W	73	A
23	W	74	C
24	X	12	C
24	X	18	C
24	X	19	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	CLM	b	9000	-	18,20,20	0.74	0	23,27,27	0.83	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	CLM	b	9000	-	-	0/22/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	b	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	2610:C	O3'	2611:C	P	1.83
1	b	2504:U	O3'	2505:G	P	1.81
1	b	2248:C	O3'	2249:U	P	1.78
1	b	1323:C	O3'	1324:G	P	1.77